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RESULT 1
Q9UMV3
ID Q9UM
AC Q9UM
DT 01-M
DT 01-M
DT 01-M
DT 01-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum
Maximum
                                                                                                                                                                      Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run
                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Listing first 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92:
   Q9UMV3;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                         Q9UMV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ned:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   number of
                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
Bd
                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length: 0
length: 2000000000
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Match
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Gapop 60.0 ,
                                                                                                                      100.0
100.0
100.0
39.0
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41
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  ) (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
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11:
12:
13:
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17:
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                                                                                                                                                                                                                                                                                                                                                                                                                              SPTREMBL_21:*
                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPLGPKWPEPVFGRLASPGF....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyright
                                                                                                                                                                                                                                                                                                                                       sp_phage:*
                                                                                                                                                                                                                                                                                                                                                sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                 sp_fungi:*
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                                                                                                                                                                                                                                                                                                                                                           sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                    sp_mammal:*
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                                                                                                                                                                                                                                                                    sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                            sp_archeap: *
                                                                                                                                                                                                                                                                                       sp_unclassified: *
                                                                                                                                                                                                                                                                                                          sp_virus:*
                                                                                                                                                                                                                                                                                                                  sp_rodent:*
                                                                                                                                                                                                                                                                                                                            sp_plant:*
                                                                                                                                                                                                                                                                                                sp_vertebrate:*
                                                                                                                                                                     Length DB
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185
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(c) 1993
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Created)
Last sequence update)
Last annotation update)
                                                                                                                     Q9UMV3
Q9ULC7
Q9UBP3
Q9UC48
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                                         PRT;
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3 - 2003
                                                                                         ALIGNMENTS
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the olos claves

the olos claves
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(without alignments)
272.514 Million cell updates/sec
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                                          B
                                                                                                                    Q9ulc7
Q9ubp3
Q9uc48
                                                                                                                                                                    Description
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homo
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ULC7
Q9ULC7;
Q1-MAY-2000
01-MAY-2000
01-JUN-2002
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NON_TER 1
SIGNAL <1
CHAIN 6
                   Takahashi M., Fujita T.;

"Partial genomic structure of human MBL-assoc!

(MASP) 2 (from exon 1 to exon 5).";

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ

1 - SIMILARITY: CONTAINS 1 CUB DOMAIN.

EMBL; AB033742; BAA86559.1; -.

EMBL; AB033742; BAA86559.1; -.
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00042; CUB; 1.
SMART; SM00179; EGF_CA; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
CCalcium-binding; EGF-like domain; Glycopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-Like.
InterPro; IPR001881; EGF_Ca.
Pfam; PF00431; CUB; 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                structural gene.";
J. Immunol. 162:3481-3490(1999).
-:- SIMILARITY: COMFAINS 1 CUB E
EMBL; Y18282; CAB50729.1; --
HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MBL-associated serine protease(MASP)-2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jensenius J.C., Schwaeble W.J.; "Two constituents of the initiation complex of the mannose-binding lectin activation pathway of complement are encoded by a single % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stover C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MASP-2
MEROPS;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MASP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; S01.229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99192764; PubMed-10092804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAp19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mannose binding lectin-associated serine
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (19kDa) precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
41; Conserv
S01.229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thiel S.,
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5
175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.

MANNOSE BINDING LECTIN-ASSOCIATED PROTEASE-2 RELATED PROTEIN, MAP19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (19KDA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                             MBL-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.8e-35;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease-2 related protein,
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                                                                                                                                            databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                             serine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protease;
                                                                                                                                                                                                             protease
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RESULT
OPERATE
Query Match
Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2)
20 EQUENCE FROM N.A.
EQUENCE FROM N.A.

AEDLINE-99262288; PubMed=10330290;
Takahashi M., Endo Y., Fujita T., Matsushita M.;
Takahashi M., Fujita T., Matsushita M.;
Takahashi M., Fujita T., Matsushita M., Fujita T., Matsushita M.;
Takahashi M., Fujita T., Matsushita M., Fujita T., Matsushita M.;
Takahashi M., Fujita T., Matsushita M., Fujita T., Matsushita M., Fujita T., Mats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UBP3;
Q9UBP3;
Q9UBP3;
Q9UBP3;
Q9UBP3;
Q9UBP3;
Q9UBP3;
Q9UBP3;
Q9UBP3;
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-UN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-UN-2002 (TrEMBLrel. 21, Last annotation update)
Mannose binding lectin-associated serine protease-2 related
Mannose binding lectin-associated serine protease 2 related
Mannose binding lectin-associated protein MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000152; A
InterPro; IPR000859; C
InterPro; IPR000561; E
InterPro; IPR001881; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00431; CUB; 1.

SMART; SM00042; CUB; 1.

SMART; SM00179; EGF_CA; 1.

PROSITE; PS0010; ASX_HYDROXYL; UNKNOWN_1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01187; EGF_CA; 1.

Calcium-binding; EGF-like domain; Glycoprotein; Protease; NON_TER 181 181

181
                            EMBL;
                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Two constituents of the initiation complex of the mannose-binding lectin activation pathway of complement are encoded by a single structural gene.";
                                                                                                EMBL;
                                                                                                                                                                     Submitted (NOV-2000) to the -!- SIMILARITY: CONTAINS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99192764; PubMed=10092804; Stover C.M., Thiel S., Thelen M., Lynch Jensenius J.C., Schwaeble W.J.;
                                                                                                                                                                                                                                         "Structure of Human MASP-2
                                                                                                                                                                                                                                                                                                                                                                          "Partial genomic structure of human MBL-associated serine (MASP)-2 (from exon 1 to exon 5)."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UBP3
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Y18281;
Y18283;
                         Y18284; CAB50731.1; -. AB008047; BAA78616.1; -. AB033742; BAA85658.1; -. Y18281; CAB50728.1; -.
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2 Gene.";
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RESULT
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01-MAY-2000
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SIGNAL 1
CHAIN 16
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InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-like.
                                                                                                    "Towards a comprehensive database of proteins patients with bladder cancer.";
J. Urol. 155:2113-2119(1996).
SEQUENCE 16 AA: 172:
                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00042; CUB; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00179; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF_2; 1.
Calcium-binding; EGF-like domain; Glycopro
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                                                                                                                                                                                 Eukaryota; Metazoa; Mammalia; Eutheria;
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01-JUN-2000
                                                                                                                                      MEDLINE=96212543; PubMed=8618346; Rasmussen H.H., Orntoft T.F., Wol
                                                                                                                                                                                                   Homo sapiens (Human)
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: 73B133D56FB229C2 CRC64;
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No.
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4e-35;
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                                                                                       Sequence 1, Application US/09874198 Patent No. US20020082208A1 GENERAL INFORMATION:
APPLICANT: Jensenius, Jens Chr.
APPLICANT: Thiel, Steffen
TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME,
TITLE OF INVENTION: USES FOR IT
                                                                                                                                                                                                                                                                                                                                                                                                           NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and is derived by analysis of the total score distribution
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/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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CURRENT APPLICATION NUMBER: US/09/874,198
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 60/042,678
PRIOR FILING DATE: 1997-04-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 41
TYPE: PRT
ORGANISM: Homo sapiens
US-09-874-198-1
                                                                                                                                                                                                                                                                                                                               RESULT 3
US-09-874-198-2
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                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Jensenius, Jens Chr.
APPLICANT: Thiel, Steffen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09874238
Patent No. US20020082209A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 41; Conservative 0
                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09874198 Patent No. US20020082208A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
TITLE OF INVENTION: MASP 2 COMPLEMENT-FIXING ENZYME, TITLE OF INVENTION: USES FOR IT FILE REFERENCE: 90911-002002 CURRENT APPLICATION NUMBER: US/09/874,198 CURRENT FILING DATE: 2001-06-04 PRIOR APPLICATION NUMBER: 09/054,218 PRIOR FILING DATE: 1998-04-02 PRIOR FILING DATE: 1998-04-03 PRIOR APPLICATION NUMBER: 60/042,678 PRIOR APPLICATION NUMBER: 60/042,678 PRIOR PILING DATE: 1997-04-03 NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/042,678
PRIOR FILING DATE: 1997-04-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/874,238
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND TITLE OF INVENTION: USES FOR IT FILE REFERENCE: 09011-002003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jensenius, Jens Chr. APPLICANT: Thiel, Steffen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 41
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                 1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
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Pred. No. 3.6e-35;
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Pred. No. 3.6e-35;
Mismatches 0;
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Qy
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; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; EENGTH: 686
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-238-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-198-2
                                                                                   В
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US-09-874-238-2
                                                                                                                                                             Query Match 100.0%; Score 41; DB 10; Length 686; Best Local Similarity 100.0%; Pred. No. 4.2e-34; Matches 41; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 41; DB 10; Length 686; Best Local Similarity 100.0%; Pred. No. 4.2e-34; Matches 41; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09874238
ent No. US20020082209A1
RAL INFORMATION:
LICANT: Jensenius, Jens Chr.
PLICANT: Thiel, Steffen
                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND TITLE OF INVENTION: USES FOR IT FILE REFERENCE: 09011-002003

CURRENT APPLICATION NUMBER: US/09/874,238

CURRENT FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: 09/054,218

PRIOR APPLICATION NUMBER: 09/054,218

PRIOR PILING DATE: 1998-04-02

PRIOR PILING DATE: 1998-04-02

PRIOR PILING DATE: 1997-04-03
completed: January 11, 2003, 11:10:13 me : 11 secs
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Maximum DB seq length: 2000000000
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tches found
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                                                 Query
Score Match Length DB ID
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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41
1 TPLGPKWPEPVFGRLASPGF......GEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262574 seqs, 29422922 residues
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                                                                                                                                   SUMMARIES
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Search completed: January 11, 2003, 11:06:46 Job time : 17 secs

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0187: 075754; Q9Y270; Q9BZH0;

30-MAY-2000 (Rel. 39, Created)

15-JUN-2002 (Rel. 41, Last annotation update)

15-JUN-2002 (Rel. 41, Last annotation update)

Mannan-binding lectin serine protease 2 precursor (EC 3.4.21.-)

(Mannose-binding protein associated serine protease 2) (MASP-2)
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
SEQUENCE FROM N.A
                                                           "A second serine protease associated with mannan-binding lectin that activates complement."; Nature 386:506-510(1997).
                                                                                                                                                       MEDIINE-97242412; PubMed-9087411; Thiel S., Jensen T.V., Stover C.M., S. Poulsen K., Willis A.C., Eggleton P., Reid K.B.M., Jensenius J.C.;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
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length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Primates;
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                                                                                                                                                                 Schwaeble W.J., Laurschwaeble W.J., Laurschwaeple W.J., Laurschwae
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(without alignments)
170.053 Million cell upd
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Compugen Ltd
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PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00032; CCP; 2.
SMART; SM00042; CUB; 2.
SMART; SM00042; EGF_CA; 1.
SMART; SM00070; Tryp_SPC; 1.
PROSITE; PS001010; ASX_HYDROXYL; 1
PROSITE; PS01180; CUB; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00135; TRYPSIN_HIS; FAI
PROSITE; PS00134; TRYPSIN_HIS; FAI
PROSITE; PS00134; TRYPSIN_HIS; FAI
PROSITE; PS00135; TRYPSIN_EGR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thiel S., Vorup-Jensen T., Stover C.M., SLIMWLL, Poulsen K., Willis A.C., Eggleton P., Hansen S., Holmskov U Reid K.B.M., Jensenius J.C.;
"Identification and characterization of a novel protein of "Identification and characterization of a ssociated serine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

-: FUNCTION: TRYPSIN PROTEASE THAT PRESUMABLY PLAYS AN IMPORTANT ROLE
-: FUNCTION: TRYPSIN PROTEASE THAT PRESUMABLY PLAYS AN IMPORTANT ROLE
-: SIMILARITY: CLEAVES C4 GENERATING C4A AND C4B.
-: SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-: SIMILARITY: CONTAINS 2 SUSHI (SCD) DOMAINS.
-: SIMILARITY: CONTAINS 2 CUB DOMAINS.
-: SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                             Pfam; PF00084; sushi; 2. Pfam; PF00089; trypsin; 1. Pfam; PF00431; CUB; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                            MIM; 605102;
                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:6902;
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EMBL; X98400; CAA67050.1; -.
EMBL; Y18287; CAB50735.1; -.
EMBL; Y18286; CAB50733.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE-99192764; PubMed=10092804; Stover C.M., Thiel S., Thelen M., Lynch N.J., Vorup-Jensen T., Jensenius J.C., Schwaeble W.J.; The constituents of the initiation complex of the mannan-binding lectin activation pathway of complement are encoded by a single
                                                                                                                                                                                                                                                                InterPro;
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InterPro; IPR000859; CUB_domain.
InterPro; IPR001314; Chymotrypsin.
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                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Park D., Kim B., Baek K., Yoon J.;
"Structure of human MASP-2 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tructural gene.";
Immunol. 162:3481-3490(1999).
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AF321558; AAG50274.1;
AF321559; AAG50274.1;
AF321560; AAG50274.1;
AF321561; AAG50274.1;
AF321561; AAG50274.1;
                                                                                                                                                                                                                                                                                                                                                                                                                              P00763;
                                                                                                                                                                                                                                                             IPR001881; EGF_Ca.
IPR001254; Ser_protease_Try.
IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                               IPR000561; EGF-like.
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      Complement
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     pathway;
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Serine protease; Protease;
                                 FALSE_NEG
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1 15
16 686
16 444
                                                                                                                                                                                                   100.0%; Score 41; DB 1; L
100.0%; Pred. No. 2.9e-34;
                          2003, 11:04:59
                                                                                                                                                                                                                                                                                                    INTERCHAIN (POTENTIAL).
POTENTIAL.
POTENTIAL.

MISSING (IN REF. 4).
L -> LCS (IN REF. 4).
G -> E (IN REF. 4).
G -> E (IN REF. 4).
MISSING (IN REF. 3).
L -> LLL (IN REF. 3).
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SUSHI 2.

SUSHI 2.

SERINE PROTEASE.

CHARGE RELAY SYSTEM (BY SIMILARITY).

HYDROXYLATION (POTENTIAL).
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                                                                                                                                                                                                                                                         Length 686;
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C:Accession: A59271
R:Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.; Poulsen, I wature 386, 506-510, 1997
A;Title: A second serine protease associated with mannan-binding lectin that activates A;Reference number: A59271; MUID:97242412; PMID:9087411
A:Accession: A59271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N;Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C;Species: Homo sapiens (man)
                                                                                                            A;Cross-references: GB:Y09926; NID:g4007626; PIDN:CAA71059.1; PID:g4007627
A;Experimental source: tissue liver
A;Experimental source: tissue liver
A;Note: submitted to GenBank, December 1996
A;Note: parts of this sequence, including the amino end of the mature prot
                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-686 <JEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
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Maximum DB seq length: 2000000000
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A;Cross-references: GDB:6071500
A;Map position: 1p36.2-1p36.3
                                                          A; Gene: GDB: MASP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
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Score Match Length DB ID
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1 TPLGPKWPEPVFGRLASPGF......GEYANDQERRWTLTAPPGYR
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Copyright (c) 1993 - 2003 Compu
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F;19-134/Domain: Clr/Cls repeat homology <ClR1>
F;142-180/Domain: EGF homology <EGFP
F;142-180/Domain: Clr/Cls repeat homology <ClR2>
F;184-293/Domain: Clr/Cls repeat homology <ClR2>
F;300-361/Domain: complement factor H repeat homology <FH1>
F;366-430/Domain: complement factor H repeat homology <FH2>
F;445-79/Domain: trypsin homology <FRY>
F;445-79/Domain: trypsin homology <FRY>
F;72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-5
F;158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;444-445/Cleavage site: Arg-Ile (autolytic) #status predicted
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F;16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
Search completed: January 11, Job time : 20 secs
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Best Local Similarity
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Pred. No. 6.7e-35;
; Mismatches 0;
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GenCore version Copyright (c) 1993 - 2003

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Minimum DB
Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ize
                                                                                                   score greater than and is derived by a
                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 2000000000
                                                                                          is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         January 11, 2003, 10:53:09; Search time 36 Seconds (without alignments) 151.758 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapop §0.0 / Gapext 60
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1 TPLGPKWPEPVFGRLASPGF......GEYANDQERRWTLTAPPGYR
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991_DAT:*
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ABG21134	AAE14568	AAE14564	AAE14565	AAE14563	NO. SCORE MATCH LENGTH DB ID	
 Novel human diagno	Human MASP-2 prote	Human MASP-2 prote	Human mature MASP-	Human 20 kDa MASP-	Description	

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ALIGNMENTS

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AAE14565
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AAE14563
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Best Local S
Matches 41
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17-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                 levels in patients suffering from e.g. infections, inflammatory disorders and spontaneous recurrent abortion. The pharmaceutical composition comprising MASP-2 inhibitor is useful for treating inflammatory disorders. The present sequence is human MASP-2 20 kDa fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of a polypeptide comprising amino acid sequence derived from mannan-binding lectin associated serine protease-2 (MASP-2) for mannan-binding lectin associated to treat bacterial, fungal,
                                AAE14565;
                                                              AAE14565 standard; peptide; 671 AA
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 39; Page 3; 76pp; English.
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01-JUN-2001; 2001DK-0000870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE14563;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to use of a polypeptide derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-179791/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (THIE/) THIEL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JENS/) JENSENIUS J C.
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                                                                                                                                                                     1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                     41 AA;
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                   100.0%; Score 41; 100.0%; Pred. No.
                                                                                                                                                                                                        0;
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                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                   1.1e-34;
                                                                                                                                                                                                                                      DB 23;
                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                      Length 41;
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                                                                                                                                                                                                      Gaps
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Human mature MASP-2 protein.

lectin

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RESULT 3
AAE14564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to use of a polypeptide derived from mannan-binding lectin (MBL) associated serine protesse-2 (MASP-2) for producing a pharmaceutical composition. MASP-2 is a complement—CC fixing enzyme and involved in lectin pathway of complement activation. The pharmaceutical composition comprising MASP-2 is useful for treating infections caused by microbes such as fungus, yeast, retrovirus (e.g. human immunodeficiency virus (HIV)), or pathogenic Dacteria which are resistant to at least one antibiotic medicament or multiresistant. The polynucleotide encoding MASP-2 is useful for treating patients deficient in MASP-2. The invention also discloses which are useful for determination of MASP-2 activity or levels in patients suffering from e.g. infections, inflammatory disorders ind spontaneous recurrent abortion. The pharmaceutical composition comprising MASP-2 inhibitor is useful for treating inflammatory disorders. The present sequence is human mature MASP-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 41; Conserv
Human MASP-2 protein
                                                                                                                                                                                    AAE14564 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JENS/) JENSENIUS J C. (THIE/) THIEL S.
                                                               17-MAY-2002
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1-JUN-2001; 2001DK-0000870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   671 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 15..671
                                                                                                                                                                                           Protein;
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on; microbe; retrovirus; HIV; abortion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 23; Pred. No. 1.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL; complement fixation; infection; microbe; retrovirus; HIV; abortion; human immunodeficiency virus; pathogenic bacteria; inflammatory disorder.
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Homo sapiens.

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Active-site
Active-site
Active-site
Use of a polypeptide comprising amino acid sequence derived from mannan-binding lectin associated serine protease-2 (MASP-2) for producing pharmaceutical composition, to treat bacterial, fungal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Encoded by CA" Misc-difference 156
                                                                                                                       (JENS/)
                                                                                                                                                                13-JUL-2000;
01-JUN-2001;
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Misc-difference 155
                                                                                            Jensenius JC,
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                                                     2002-179791/23
DB; AAD24224.
                                                                                                                       JENSENIUS J C.
THIEL S.
                                                                                                                                                                2000DK-0001089.
2001DK-0000870.
                                                                                              Thiel
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483
532
633
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of peptides"
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16..31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label= Clr/Cls-like_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complement control protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Encoded by
                                                                                                                                                                                                                                                                                                                                                      "Linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "This
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Fragment obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "This region is specifically claimed in
                                                                                                                                                                                                                                                                                                                             Serine_protease_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCP-2_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCP-1_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region is specifically claimed in claim 41.0 to 296 is specifically claimed in claim 47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is specifically claimed in claim 46"
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Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to use of a polypeptide derived from mannan-binding lectin (MBL) associated serine protease-2 (MASP-2) for producing a pharmaceutical composition. MASP-2 is a complement-fixing enzyme and involved in lectin pathway of complement activation. The pharmaceutical composition comprising MASP-2 is useful for treating infections caused by microbes such as fungus, yeast, retrovirus (e.g. human immunodeficiency virus (HIV)), or pathogenic bacteria which are resistant to at least one antibiotic medicament or multiresistant. The polynucleotide encoding MASP-2 is useful for treating patients deficient in MASP-2. The invention also discloses MASP-2 assays which are useful for determination of MASP-2 activity or the polynucleotide for determination of MASP-2 activity or the pathogeness of the
                                                                                                                                                                                                                                                                                                                                                                                 /note= "Encoded by Misc-difference 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL; complement fixation; infection; microbe; retrovirus; HIV; abortion; human immunodeficiency virus; pathogenic bacteria; inflammatory disorde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE14568 standard; Protein; 686
                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                               /note= "Encoded Misc-difference 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human MASP-2 protein, alternative version.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      levels in patients suffering from e.g. infections, inflammatory disorders and spontaneous recurrent abortion. The pharmaceutical composition comprising MASP-2 inhibitor is useful for treating inflammatory disorders. The present sequence is human MASP-2 protein.
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                      13-JUL-2000; 2000DK-0001089
01-JUN-2001; 2001DK-0000870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                       13-JUL-2001; 2001WO-DK00499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ote: The present sequence is stated as being the same as EQ ID NO:2 shown in sequence listing of the specification (AAE14568) However the sequences differ at various locations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            omo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        686 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155
                                                                                                                                                                                                                                                                                              /note- "Encoded by CAG" 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Signal_peptide 16..686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Mature_MASP-2_protein
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Pred. No. 1.2e-33;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               retrovirus (e.g. human immunodeficiency virus (HIV)), or pathogenic bacteria which are resistant to at least one antibiotic medicament or multiresistant. The polynucleotide encoding MASP-2 is useful for treating patients deficient in MASP-2. The invention also discloses MASP-2 assays which are useful for determination of MASP-2 activity or levels in patients suffering from e.g. infections, inflammatory disorders and spontaneous recurrent abortion. The pharmaceutical composition comprising MASP-2 inhibitor is useful for treating inflammatory disorders. The present sequence is human MASP-2 protein. Note: The present sequence is stated as being the same as SEQ ID NO:2 shown in figure 6 of the specification (AAE14564).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to use of a polypeptide derived from mannan-binding lectin (MBL) associated serine protease-2 (MASP-2) for producing a pharmaceutical composition. MASP-2 is a complement-fixing enzyme and involved in lectin pathway of complement activation. The pharmaceutical composition comprising MASP-2 is useful for treating infections caused by microbes such as fungus, yeast,
                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 41; Page 71-73; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of a polypeptide comprising amino acid sequence derived from mannan-binding lectin associated serine protease-2 (MASP-2) for producing pharmaceutical composition, to treat bacterial, fungal,
            Drmanac RT, Liu C,
                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #21125
                                                                                                                                                                                                                                                                                                                                                                                                                  ABG21134 standard; Protein; 1034 AA
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                                                                              31-MAR-2000;
23-AUG-2000;
                                                                                                                              30-MAR-2001; 2001WO-US08631
                                                                                                                                                               11-OCT-2001
                                                                                                                                                                                                                                                                                                                                               18-FEB-2002 (first entry)
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(THIE/) THIEL S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    686 AA;
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                                                                              2000US-0540217
2000US-0649167
            Tang
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cc polymeride (II) sequences. (I) is useful as hybridisation probes, cc polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tags (CC for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical maging of sites expressing (II). (I) and (II) are useful for treating isorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations in CC diagnostic genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC and to produce other types of data and products dependent on DNA and CC anino acid sequences. ABG00010-ABG30377 represent novel human CC Note: The sequence data for this pattent did not appear in the printed specification, but was obtained in electronic format directly from WIPO CC at tftp.wipo.int/pub/published_pct_sequences.
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Search completed: January 11, 2003, 11:04:36 Job time : 36 secs
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Best Local Similarity 100.0%;
Matches 41; Conservative 0
                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73.
N-PSDB; AAS85321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and
                                                                                                     752 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 792
                                                                                                                             1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                 1034 AA;
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Pred. No. 1.7e-33;
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                                                                                                                                                                                                                                                        Length 1034;
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Result
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Maximum Match 100%
Listing first 60 summaries
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Maximum DB seq
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1: /cgn2_6/ptodata/2/pubpaa/U
2: /cgn2_6/ptodata/2/pubpaa/U
3: /cgn2_6/ptodata/2/pubpaa/U
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5: /cgn2_6/ptodata/2/pubpaa/U
6: /cgn2_6/ptodata/2/pubpaa/U
6: /cgn2_6/ptodata/2/pubpaa/U
6: /cgn2_6/ptodata/2/pubpaa/U
9: /cgn2_6/ptodata/2/pubpaa/U
11: /cgn2_6/ptodata/2/pubpaa/U
11: /cgn2_6/ptodata/2/pubpaa/U
13: /cgn2_6/ptodata/2/pubpaa/U
14: /cgn2_6/ptodata/2/pubpaa/U
15: /cgn2_6/ptodata/2/pubpaa/U
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17: /cgn2_6/ptodata/2/pubpaa/U
18: /cgn2_6/ptodata/2/pubpaa/U
19: /cgn2_6/ptodata/2/pubpaa/U
11: /cgn2_6/ptodata/2/pubpaa/U
12: /cgn2_6/ptodata/2/pubpaa/U
13: /cgn2_6/ptodata/2/pubpaa/U
14: /cgn2_6/ptodata/2/pubpaa/U
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length: 2000000000
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Gapop 10.0 ,
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238
1 TPLGPKWPEPVFGRLASPGF......GEYANDQERRWTLTAPPGYR 41
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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US-10-004-551-18
US-10-004-551-20
US-10-004-551-24
 US-09-799-118-6
US-09-925-302-611
US-09-919-497-89
US-09-874-198-7
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Sequence 1, Appli
Sequence 2, Appli
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Sequence 5, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 10, Appli
Sequence 20, Appli
Sequence 21, Appli
Sequence 24, Appli
Sequence 14, Appli
Sequence 16, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 7, Appli
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Score 238; DB 10; pred. No. 5.1e-22; 0; Mismatches 0;	4198 PLEMENT-FIXING ENZYME, IT (709/874,198 04 54,218 42,678 Version 4.0	ALIGNMENTS	US-09-874-238-7 US-09-808-602-94 US-09-925-310-1282 US-09-925-310-1416 US-09-925-310-1416 US-09-925-311-1024 US-09-874-198-8 US-09-874-198-8 US-09-87-593-6 US-09-887-593-7 US-09-987-988-104 US-09-997-881-104 US-09-997-881-104 US-09-998-998-104 US-09-998-104-40-4 US-09-988-104-40-4 US-10-087-422-13 US-09-888-602-986 US-09-888-602-986 US-09-888-602-986
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RESULT 4
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                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 686
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09874198 Patent No. US20020082208A1
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Best Local Similarity
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RENT APPLICATION NUMBER: US/09/874,198
RRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 60/042,678
PRIOR FILING DATE: 1998-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jensenius, Jens Chr. APPLICANT: Thiel, Steffen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/874,238
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
PRIOR FILING DATE: 1998-04-02
OR APPLICATION NUMBER: 60/042,678
OR FILING DATE: 1997-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING TITLE OF INVENTION: USES FOR IT
                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING TITLE OF INVENTION: USES FOR IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jensenius, Jens Chr. APPLICANT: Thiel, Steffen
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                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Homo sapiens
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TYPE: PRT
                                                                                                                                               Local
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                                                    TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 56
                                                                                                                                41;
                                                                                                                                               Similarity
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Pred. No. 1.1e-20;
Mismatches 0;
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Pred. No. 5.1e-22;
, Mismatches 0;
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; NAME/KEY: SITE
; LOCATION: (70)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-563
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US-09-874-198-6
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APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06
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Matches
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LENGTH: 174
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LENGTH: 686
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                                                                                                                                         Matches
                                                                                                                                                                        Query Match
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CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 09011-002003
CURRENT APPLICATION NUMBER: US/09/874,238
CURRENT FILING DATE: 2001-06-04
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PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 60/042,678
PRIOR FILING DATE: 1997-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, TITLE OF INVENTION: USES FOR IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jensenius, Jens Chr. APPLICANT: Thiel, Steffen
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                        Similarity
                                                                                                                                       Conservative
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                                                                                                                                                      Score 93.5; DB 10 Pred. No. 0.00028;
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Pred. No. 1.1e-20;
; Mismatches 0;
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Sequence 6, Application US/09874198 Patent No. US20020082208A1 GENERAL INFORMATION:

APPLICANT: Jensenius, Jens Chr. APPLICANT: Thiel, Steffen

TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, TITLE OF INVENTION: USES FOR IT

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RESULT 8
US-10-004-551-18
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                                                                                                                                                                                                 Sequence 18, Application US/10004551
Publication No. US20030004310A1
GENERAL INFORMATION:
APPLICANT: SHIMEDTS, RICHARD A
APPLICANT: FERNANDES, ELMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 14; Conserv
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SEQ ID NO 6
LENGTH: 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND ITTLE OF INVENTION: USES FOR IT FILE REFERENCE: 09011-002003
CURRENT APPLICATION NUMBER: US/09/874,238
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 60/042,678
                                                           APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
CURRENT APPLICATION NUMBER: US/10/004,551
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR EPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
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CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
PRIOR FILING DATE: 1998-04-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 679
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Pred. No. 0.0014;
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US-10-004-551-22
Sequence 22, Application US/10004551
Publication No. US20030004310A1
GENERAL INFORMATION:
APPLICANT: SHIMKETS, RICHARD A
APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
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Best Local Similarity
Watches 21; Conserve
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                                                                                                                     US-10-004-551-22
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: LENGTH: 525
: TYPE: PRT
                                                                                                                                                 SOFTWARE: PatentIn Ver.
SEQ ID NO 22
LENGTH: 525
TYPE: PRT
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CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
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PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
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CURRENT FILING DATE: 2001-12-05
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les 21; Conserv
5 PKW--PEPV-------FGRLASPGFPGEYANDQERRWILTAPPGYR 41
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                                                                Score 91.5; DB 9
Pred. No. 0.0016;
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Pred. No. 0.0016;
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Pred. No. 0.0016;
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RESULT 13
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                    Sequence 16, Application US/10004551
Publication No. US20030004310A1
GENERAL INFORMATION:
APPLICANT: SHIMKETS, RICHARD A
APPLICANT: FERNANDES, ELMA
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CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
"MBER OF SEQ ID NOS: 110
TWARE: Patentin Ver. 2.1
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APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: 15966-559
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APPLICANT: FERNANDES, ELMA
APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
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PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
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CURRENT FILING DATE: 2001-12-05
APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
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THER INFORMATION: n 2093 can be A,
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Pred. No. 0.0032;
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Pred. No. 0.0016;
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US-10-041-406-5
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US-09-886-429-4
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                  SEQ ID NO 5
LENGTH: 144
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                                                                                                                                                                                                                                                                               Sequence 5, Application US/10041406 Patent No. US20020164705A1
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SEQ ID NO 16
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                                                                                                                                    FILE REFERENCE: 10448-130001
CURRENT APPLICATION NUMBER: US/10/041,406
CURRENT FILING DATE: 2002-01-08
                                                                                                                                                                                    TITLE OF INVENTION: 39362, A NOVEL CUB DOMAIN CONTAINING TITLE OF INVENTION: PROTEIN FAMILY MEMBER AND THE FILE PREFERNORS. AND THE PROPERTY OF THE PREFERNORS.
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CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/213,963
PRIOR FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 56739, A NOVEL CUB DOMAIN CONTAINING
TITLE OF INVENTION: PROTEIN AND USES THEREOF
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CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
                                                                                                 PRIOR APPLICATION NUMBER: 60/: PRIOR FILING DATE: 2001-01-08
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                                                          SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                NUMBER OF SEQ ID NOS: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 16
US-09-799-118-6
                                                                                                                                                                                                                                       US-09-799-118-6
Sequence 611, Application US/09925302 Patent No. US20020044941A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09799118
Patent No. US20020090708A1
**ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 34.7
Best Local Similarity 50.0
Matches 17; Conservative
                                                                                                                                                                      Matches
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 GTITSPNYPNSPSGESYPNNLECVWTISAPPGYR 49
                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 GRLASPGFP----GE-YANDQERRWTLTAPPGYR 41
                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,118
FILING DATE: 06-Mar-2001
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lee, Tae Ho
Wisniewski, Hans Georg
                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Cytokine-Induced Protein,
Therefor and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                PQKLFGEVTSPLFPKPYPNNFETTTVITVPTGYR 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/242,097 FILING DATE: 13-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                    LENGTH: 101 amino acids
                                                                                                                                                                    Conservative
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                                                                                                                                                                                  34.0%;
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50.0%;
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Pred. No. 0.0047;
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Pred. No. 0.006;
5; Mismatches
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                                                                                                                                                                                                  DB 10; Length 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suite 300
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RESULT 19
US-09-874-198-7
: Sequence 7, Application US/09874198
: Patent No. US20020082208A1
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Sequence 89, Application US/09919497
Patent No. US20020106662A1
GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic Acids, Proteins an:
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR TILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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                                GENERAL INFORMATION:
APPLICANT: Jensenius, Jens Chr.
APPLICANT: Thiel, Steffen
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LENGTH: 449
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LENGTH: 351
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TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND TITLE OF INVENTION: USES FOR IT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MUTTER, GEORGE L. TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR EILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: B0801/7225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE LOCATION: (335)
OTHER INFORMATION: Xaa equals any of the naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE LOCATION: (307)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 44.18;
hes 15; Conservation
                                                                                                                                                                                                                       28 PNYTRPVFLCGGDVKGESGYVASEGFPNSYPPNKECIWTITVPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 POKLEGEVTSPLFPKPYPNNFETTTVITVPTGYR 56
                                                                                                                                                                                                                                                         5 PKWPEPVF------GRLASPGFPGEYANDQERRWTLTAPPG 39
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                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 0.023;
5; Mismatches
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Pred. No. 0.018;
5; Mismatches
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Sequence 7, Application US/09874238

Patent No. US20020082209A1

GENERAL INFORMATION:
APPLICANT: Thiel, Steffen

TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND TITLE OF INVENTION: USES FOR IT

FILE REFERENCE: 09011-002003

CURRENT FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: US/09/874,238

CURRENT FILING DATE: 1997-04-02

PRIOR APPLICATION NUMBER: 60/042,678

PRIOR APPLICATION NUMBER: 60/042,678

PRIOR FILING DATE: 1997-04-03

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 688

TYPEE: PRT

ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/874,198
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 60/042,678
PRIOR FILING DATE: 1997-04-03
NUMBER OF SEQ ID NOS: 8
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 688
TYPE: PRT
ORGANISM: Homo sapiens
US-09-874-198-7
Search completed: January 11, 2003, 11:03:49 Job time: 61 secs
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US-09-874-238-7
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Best Local Similarity 44.1%;
Matches 15; Conservative
                                                                                                                                                                ery Match 34.0%;
Local Similarity 44.1%;
hes 15; Conservative
                                                                                5 POKLEGEVTSPLEPKPYPNNEETTTVITVPTGYR 38
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries
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Maximum DB seq length: 2000000000
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       65.5
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63
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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238
1 TPLGPKWPEPVFGRLASPGF......GEYANDQERRWTLTAPPGYR
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Copyright (c) 1993 - 2003
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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US-08-242-997-6
US-08-839-008-9
US-08-839-008-9
US-08-839-008-5
US-08-839-008-7
US-08-839-008-7
US-08-839-008-7
US-09-374-135-6
US-09-374-135-7
US-09-374-135-7
US-09-374-135-7
US-08-872-757-2
US-08-872-757-2
US-08-872-757-3
US-08-872-757-3
US-08-872-757-3
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US-08-872-757-3
US-08-872-757-3
US-08-872-757-3
US-08-872-757-3
US-08-872-757-3
US-08-866-650-5
US-09-3432-473-5
US-09-321-287-3
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US-09-032-523-2
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-08-471-770-	8-470-202-	-09-134-001C	8-675-140-	-08-675-140	8-534-342-	8-534-342-	22-171-	-08-922-171-	-08-494-168-1	6 - 119	-09-000-179-	9-206-69	97-	8-024-868-	-341-587-	-09-341-587-	-09-548-608-2	-09-570-573-2	-09-500-811-2	8-963-825-2	-08-931-820-	8-936-135-1	-08-936-135-1	-08-936-135-	-135-1	8-936-135-	-08-936-135-	6-135-	8-936-135-	-08-936-135	9-116-473-	US-08-936-135-18
equence 46,	Sequence 46, Appl	equence 2869, A	equence 6, App	e 5, App	e 6, App	e 5, App	O	e 3, 7	e 10,	e 1, App	e 1,	e 2,	e 2,	@ 22 ,	Θ ω '	e 1, A	e 21,	e 21,	ი 2	e 21,	Ø	equence 16,	equence 14,	e 12,	equence	ი 8,	e 24,	e 22,	e 20, Ap	o 6,	e 4, App	Sequence 18, Appl

ALIGNMENTS

RESULT 1 US-08-470-350B-2 Sequence 2, Application US/08470350B Patent No. 5684126 GENERAL INFORMATION:
APPLICANT: L1, xiao
APPLICANT: Styder, Solomon H
TITLE OF INVENTION: Ebnerin: A Secreted von
TITLE OF INVENTION: Protein Associated with
NUMBER OF SEQUENCES: 6 CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WOLIFE, SUSAN A
REGISTRATION NUMBER: 33,568
REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100 TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,350B COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CORRESPONDENCE ADDRESS: COUNTRY: ZIP: 200 TELEPHONE: 202-508-9299 STREET: 1001 G St CITY: Washington STATE: D.C. FILING DATE: ADDRESSEE: Banner & Witcoff, Ltd. STREET: 1001 G Street, N.W. 20001 USA 01107.48790 Ebner's Gl Taste Buds

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US-09-206-695-6
; Sequence 6, Applicatio
; Sequent No. 6210905
; Patent No. 6210905
; GENERAL INFORMATION:
; APPLICANT: Lee, Tal
; APPLICANT: Wisniew
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                                                                                                       RESULT 3
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Best Local Similarity
Matches 15; Conserv
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Patent No. 5846763
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,097
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25.618
REGISTRATION NUMBER: 25.618
                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: LE TELECOMMUNICATION INFORMATION: TELEPHONE: 212-628-5197
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT: Lee, Tae Ho
PPLICANT: Wisniewski, Hans Georg
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding
TITLE OF INVENTION: Therefor and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cli.
STATE: D..
STATE: 20004
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TELEFAX: 212-737-3528
ORMATION FOR SEQ ID NO:
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CITY: V
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                                                                                                                                                                                      PEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
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                                                                    Application US/09206695
                                                                                                                                                                                                                                                                                                                                                                           101 amino acids
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419 Seventh Street, N.W.,
   Wisniewski, Hans Georg
                                                                                                                                                                                                                        Conservative
                   Lee, Tae Ho
                                                                                                                                                                                                                                                                                                                            linear
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Pred. No.
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Pred. No. 0.022;
5; Mismatches 17;
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0.0027;
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                                                                                                                                                                                                                                                                                                                                            Patent No.
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Best Local
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                                                                                                                                                                                                                                                 APPLICANT:
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                            APPLICANT: Yue, Tian-Li
TITLE OF INVENTION: Smooth Muscle Cell-Derived Migration Factor
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/242,097 FILING DATE: 13-MAY-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                           COUNTRY:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 419 Sever CITY: Washington
                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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TELEFAX: 212-737-3528
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Young, Peter R
Yue, Tian-Li
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419 Seventh Street, N.W., Suite 300
                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Rosen, Craig A
                                                                                                                                                                                                                                                                                            McDonnell,
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US-08-839-008-2
; Sequence 2, A
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TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                            TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS.
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Young, APPLICANT: Yue, Ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 28-NOV-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                    APPLICATION NUMBER: 08/50 FILING DATE: 28-NOV-1995 ATTORNEY/AGENT INFORMATION:
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CITY: F
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TOPOLOGY: lir
                                            REFERENCE/DOCKET NUMBER: P50
"LECOMMUNICATION TOTAL
                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 23-APR-1997
                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Baumeister, Kirl
REGISTRATION NUMBER:
                                                                         NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                             COMPUTER:
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17; Conserv
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McNulty, Dean E
Rosen, Craig A
Siemens, Ivo
Young, Peter R
Yue, Tian-Li
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                            Smooth Muscle Cell-Derived Migration Factor
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ean E
                                                                                                                                    08/563,697
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Pred. No.
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CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER APPLICATION NUMBER: 60/051,932
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EARLIER APPLICATION NUMBER: 60/05
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/05
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/05
EARLIER FILING DATE: 1997-07-08
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Patent No. 634258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: 123 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fischer et al
                                          EARLIER APPLICATION NUMBER: EARLIER FILING DATE: 1997-0
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TOPOLOGY: lin
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/0
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                    APPLICATION NUMBER:
                                                                                                        APPLICATION NUMBER:
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FILING DATE: 1997-08-18
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1997-07-08
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                                                              60/055,949
                                                                                                        60/055,948
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                    60/055,953
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APPLICATION NUMBER: 60/ FILING DATE: 1997-08-18 APPLICATION NUMBER: 60/ FILING DATE: 1997-08-18

60/055,964 8-18 60/056,360

APPLICATION NUMBER: 60/055,947 FILING DATE: 1997-08-18

APPLICATION NUMBER: 60/055,684

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Best Local Similarity
Satches 15; Conserva
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US-08-839-008-5
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                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hurle, I APPLICANT: McDonne APPLICANT: McDonne APPLICANT: McNulty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (26)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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V ID NO 363

LENGTH: 52

TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
             MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                              NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCATION:
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                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                  APPLICANT: Yue, Tit
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                       nt No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIER FILING DATE: 1997-09-12
BER OF SEQ ID NOS: 672
                                                                                                                  COUNTRY: US
ZIP: 19406
                                                                                                                                                                   ADDRESSEE: Smiling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 FGRLASPGFPGEYANDQERRWTLTAPPGY 40
APPLICATION NUMBER:
                                                                                                                                               CITY: King of Prussia
STATE: PA
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APPLICATION NUMBER: 60/
FILING DATE: 1997-09-12
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FILING DATE: 1997-08-18
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                                                                                                                                                                                                                                                              Siemens, Ivo R
Young, Peter R
Yue, Tian-Li
                                                                                                                                  USA
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McNulty, Dean E
Rosen, Craig A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                  Smooth Muscle Cell-Derived Migration Factor
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51.7%;
us/08/839,008
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Pred. No.
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Best Local Similarity
Matches 16; Conserv?
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             TELEFAX: 610-270-5090 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                             REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/563,697
                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
SEQUENCE CHARACTERISTICS:
                                                                                                            FILING DATE: 28-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: li
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yue, Tian-Li
TITLE OF INVENTION: Smooth Muscle Cell-Derived Migration Factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                             TELEPHONE:
                                                                                             NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                              APPLICATION NUMBER:
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ZIP: 19406
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STATE: PA
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CLASSIFICATION:
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McNulty, Dean E
Rosen, Craig A
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Young, Peter R
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                                             610-270-5096
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-839-008-7
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US-09-032-523-8
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                                                                                                                           ; CLONE:
US-09-032-523-8
                                                                           Query Match
Best Local 9
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Best Local Similarity
Matches 16; Conserv
                                                              Matches
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPHONE: 650-845-4166
                                                                                                                                                                                                                                                                    TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quence 8, Application US/09032523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FASTSEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NITHTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl
APPLICANT: Baugh, Mariah
TITLE OF INVENTION: HUMAN PROTEINASE MOLECULES
NUMBER OF SEQUENCES: 9
                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NERAL INFORMATION:
APPLICANT: Bandma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ent No.
                                                                                                                              MEDILL
LIBRARY: Gen-
CAME: 2589009
                                                                                                                                                                                                  LENGTH: 468 amino
TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3174 Por CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
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STRANDEDNESS: si
27 PNYTRPVFLCGGDVTGESGYVASEGFPNLYPPNKKCIWTITVPEG 71
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                          5 PKWPEPVF-----GRLASPGFPGEYANDQERRWTLTAPPG 39
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linear
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35.6%;
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                                                         Score 74; DB 4; Length 468; Pred. No. 0.11; Indels
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; SOFTWARE: Patent:
; SEQ ID NO 6
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Mouse
US-09-374-135-6
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US-09-374-135-6
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,757
FILING DATE: 10-JUN-1997
CLASSIFICATION 2435
PRIOR APPLICATION UMBER: US/08/609,187
APPLICATION NUMBER: US/08/609,187
APPLICATION NUMBER: US/08/609,187
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-028-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/374,135
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/095,982
PRIOR FILING DATE: 1998-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: BPC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND TITLE OF INVENTION: SECRETED BY PROSTATE AND BLADDER CANCER CELLS FILE REFERENCE: 1703-017.US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS: ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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tes 13; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1155 Ave
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 10036-2711
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Leong, Kahan
Raitan-
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Saffran, Douglas C.
Jakobovits, Aya
                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sieron, Aleksander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hojima, Yoshio
Li, Shi-Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prockop, Darwin J.
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                                                                                                                ; MOLECULE TYPE: US-08-572-225-1
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best Local Similarity 44.8%;
Matches 13; Conservation
                                                                    Query Match
Best Local Similarity
                                                         Matches
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEPAX: 415-854-3694
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 13-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ent No.
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                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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402 GSITSPGWPKEYPPNKNCIWQLVAPTQYR 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    572-225-1
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
operating SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                          TYPE: amino acid
STRANDEDNESS: un
TOPOLOGY: unknow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1155 AVCITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York
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TOPOLOGY: linear
                                                                                                                                                                                        LENGTH:
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66141 PENNIE
FOR SEQ ID NO:
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                                                                                                                                                                                        788 amino acids
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                                                                                                                                            unknown
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                                                                                                                            protein
                                                                                                                                                            unknown
                                                                      29.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Darwin J.
                                                                                                                                                                                                                                                                                                                                                                                US/08/572,225
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                                                                                                                                                                                                                                                                                            8389-031
                                                                      Score 69;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
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                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 0.8
                                                                      DB 1;
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                                                                                  Length 788;
                                                        Indels
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                                                      0;
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                                                     Gaps
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; LENGTH: 102
; TYPE: PRT
; ORGANISM: Mouse
US-09-374-135-7
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US-09-374-135-7
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Best Local Similarity
Matches 10; Conserv
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SEQ ID NO 7
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/374,135
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/095,982
PRIOR FILING DATE: 1998-08-10
NUMBER OF SEQ ID NOS: 20
           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/034,471

FILING DATE: 02-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F

REGISTRATION NUMBER: 23,031

REFERENCE/POCKET NUMBER: ATG-500

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jakobovits, Äya
TITLE OF INVENTION: BEC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND
TITLE OF INVENTION: SECRETED BY PROSTATE AND BLADDER CANCER CELLS
FILE REFERENCE: 1703-017.US1
                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ARLETH, ANTHONY J. APPLICANT: WILLETTE, ROBERT N. APPLICANT: ELSHOURBAGY, NABIL A. APPLICANT: LI XIAOTONG TITLE OF INVENTION: HUMAN CARDIA TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                      COUNTRY:
ZIP: 19
                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                       STREET: P.O. BOX 91
CITY: VALLEY FORGE
STATE: PA
                                                                                                                                                                                                      APPLICATION NUMBER: US/08/991,408
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TELEPHONE:
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o. 6277972
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Leong, Kahan
Raitano
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Saffran, Douglas C.
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                                                                                                                                                                                                                                                                                                                                                       USA
610-407-0700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN CARDIAC/BRAIN TOLLOID-LIKE
                                  ATG-50038
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0.12;
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TELEFAX:

610-407-0701

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                                                                                                                                                                                                                                                                                                      RESULT 16
US-08-872-757-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-991-408-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 4
LENGTH: 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN FILE REFERENCE: ATG-50038-D1
CURRENT APPLICATION NUMBER: US/09/432,473
.CURRENT FILING DATE: 1999-11-01
EARLIER APPLICATION NUMBER: 08/991,408
EARLIER APPLICATION NUMBER: 08/991,408
EARLIER FILING DATE: 1997-12-16
                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08872757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                               GENERAL INFORMATION:

APPLICANT: Prockop, Darwin J.

APPLICANT: Hojima, Yoshio

APPLICANT: Li, Shi-Wu

APPLICANT: Sieron, Aleksander

TITLE OF INVENTION: PROCESSES; METHODS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/034,471 EARLIER FILING DATE: 1997-01-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ELSHOURBAGY, NABIL A. APPLICANT: LI, XIAOTONG
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                                                                                                     NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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Local Similarity 37.9%;
ses 11; Conservative
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STRANDEDNESS: sir
                  COUNTRY:
                                     CITY: New York STATE: New Yor
                                                                    STREET:
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                                                                                     ADDRESSEE:
10036-2711
                                 New York
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Pred. No. 0.85;
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; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-872-757-4
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Best Local S
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TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                              NAME: Berson, Bennett J
REGISTARION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-51-5000
                                                                                                    APPLICATION NUMBER: US/08
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           756 GTITSPNWPDKYPSKKECTWAISSTPGHR 784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                 STATE:
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10; Conserv
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Takahara, Kazuhiko
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10-JUN-1997
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Pred. No. 1
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WILLETTE, ROBERT N.

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, TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-866-650-5
                                                            US-08-991-408-2
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                                                                            RESULT 19
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             Sequence 2, Application US/08991408 Patent No. 6008017 GENERAL INFORMATION:
                                                                                                                                                                                       Matches
                                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
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PPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                               TELEFAX: 608-251-9166
CORMATION FOR SEQ ID NO:
                                                                                                                          783 GLITSPNWPDKYPSRKECTWEISATPGHR 811
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                                                                                                                                                                                                                                                                               LENGTH: 1013 amin
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                    13 GRLASPGFPGEYANDQERRWTLTAPPGYR 41
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                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Berson, Bennett
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Madison
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ARLETH, ANTHONY J.
                                                                                                                                                                                       Conservative
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Pred. No.
                                                                                                                                                                                                     Score 68;
Pred. No.
                                                                                                                                                                                       Mismatches
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; TOPOLOGY: 1:; MOLECULE TYPE: US-08-991-408-2
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                                                                                                                                                                                                                                                                                       RESULT 20
                                                                                                                                                                                                                                            Sequence 5, Application US/09240473 Patent No. 6297011
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                    APPLICANT:
APPLICANT:
                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                       APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: AT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 02-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 01.09
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                                                                                                                                                                                                                                                                                                                                 783 GLITSPNWPDKYPSRKECTWEISATPGHR 811
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                STREET: 1 Sout
CITY: Madison
                                                                                                   ADDRESSEE: Quaries ... Street
                                                                                                                                                                                                                                                                                                                                                            13 GRLASPGFPGEYANDQERRWTLTAPPGYR 41
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CITY: VALLEY FORGE
                                                          ZIP:
                                                                     COUNTRY:
                                                                                    STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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Takahara, Kazuhiko
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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LI, XIAOTONG
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37.9%;
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for Windows Version
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                                                                                                                                                                                                                 Daniel S
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                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 68;
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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PatentIn Release #1.0,

Version #1.30

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CURRENT APPLICATION NUMBER: US/09/240,473

FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.93839

TELEPHONE: 608-251-5000
TELEPAX: 608-251-5166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1013 amino acids
TYPE: amino acid
TYPE: maino acid
TYPE: protein
US-09-240-473-5

Y Match
Local Similarity 37.9%; prod. No. 1.6;
LOcal Similarity 37.9%; prod. No. 1.6;
LOcal Similarity 9%; prod. No. 1.6;
LOcal Similarity 9%; prod. No. 1.6;
Oy 13 GRLASPGFFGEYANDOERRUTLTAPPGYR 41
Db 783 GLITSPNWPDKYPSRKECTWEISATPGHR 811
Search completed: January 11, 2003, 10:54:19
Job time: 68 secs
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Title:
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                                                                                                                                                                   Perfect score:
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number of hits satisfying chosen parameters:
                                                                                  BLOSUM62
Gapop 10.0 ,
                                                                                                                                         US-09-874-198-1
238
1 TPLGPKWPEPVFGRLASPGF......GEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                    January 11, 2003, 10:44:28; Search time 66 Seconds
                                              283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.3 Compugen Ltd
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59.720 Million cell updates/sec
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Minimum I Maximum I

DB seq

length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 60 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	ò			) J	2		NO.	Result
65.5	65.5	Š	6	67	67.5	<u>с</u>	68	68	89	69	69	69	69	69	71.5	72	72.5	74	74	74.5	78	80.5	က	81	83.5	85	93	238	Score	
						•	28.6	•	•									•			•	•	٠		•		39.1	100.0	Match	% Query
920	171	77	0	288	694	2083	1594	767	504	1464	991	986	823	730	1070	3623	695	402	319	889	3623	977	705	449	1290	610	699	686	Length	
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57.5	57.5	57.5	57.5	57.5	57.5	58	58	58	58	58	58	58.5	59	59	59	59.5	60	60	60	60.5	60.5	61	62	62	63	63	63	63	65	65
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1691	1497	349	277	275	223	2403	1670	1464	381	347	105	161	1051	636	511	1433	1466	418	418	886	271	294	980	980	1669	1524	391	343	3871	1057
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## ALIGNMENTS

R:Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.; Poulsen, Nature 386, 506-510, 1997
A;Title: A second serine protease associated with mannan-binding lectin that activate A;Reference number: A59271; MUID:97242412; PMID:9087411
A;Accession: A59271 Ra-reactive factor (EC 3.4.21.-) 2 precursor - human
N;Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C:Species: Homo sapiens (man)
C:Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 16-Jun-2000 .
C:Accession: A59271 A; Molecule type: mRNA A; Residues: 1-686 < JEN> A;Cross-references: GB:Y09926; NID:g4007626; PIDN:CAA71059.1; PID:g4007627 A; Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Experimental source: tissue liver A;Note: submitted to GenBank, December 1996 A;Note: parts of this sequence, including the amino end of the mature protein, were C;Genetics:

C;Genericus
A;Genericus
A;Genericus
A;Genericus
A;Genericus
A;Cross-reterences: GDB:6071500
A;Cross-reterences: GDB:6071500
A;Cross-reterences: GDB:6071500
A;Map position: lp36.2-lp36.3
C;Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement facto
C;Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serin
F;1-15/Domain: signal sequence #status predicted <SIC>
F;16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F;19-134/Domain: C1r/C1s repeat homology <CIR1>
F;142-180/Domain: C1r/C1s repeat homology <CIR1>
F;360-361/Domain: Complement factor H repeat homology <FH1>
F;366-430/Domain: complement factor H repeat homology <FH2>
F;366-430/Domain: trypsin homology <TRY>
F;72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-5
F;159/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:444-445/Cleavage site: Arg-IIe (autolytic) #status predicted
F:444-445/Cleavage site: Arg-IIe (autolytic) #status predicted

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C;Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement fac C;Superfamily: complement subcomponent pathway; duplication; glycoprotein; E;1-17/Domain: signal sequence #status predicted <SIG>
F;18-448,449-699/Product: Ra-reactive factor #status predicted <MAT>
F;19-135/Domain: C1r/C1s repeat homology <C1R1>
                                                 hypothetical protein R151.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #: C;Accession: T16761
                                                                                                                                                                                                                                             Db
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A;Cross-references: DDBJ:D17525; NID:g439712; PIDN:BAA04477.1; PID:g439713
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Takada, F.; Takayama, Y.; Hatsuse, H.; Kawakami, M. Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
A;Title: A new member of the C1s family of complement proteins found A;Reference number: JN0883; MUID:94059062; PMID:8240317
A;Accession: JN0883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:D28593; NID:g790963; PIDN:BAA05928.1; PID:g471128 R;Takada, F.; Takayama, Y.; Hatsuse, H.; Kawakami, M. Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Sato, T.; Endo, Y.; Matsushita, M.; Int. Immunol. 6, 665-669, 1994
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       submitted
                             R; Fulton,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: GDB: MASP1; GDB: CRARF; CRARF1; PRSS5; MASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N; Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ra-reactive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :Comment: This is a serum bactericidal factor that activates complement C4 and
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 159/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted 448-449/Cleavage site: Arg-Ile (autolytic) #status predicted 490,552,646/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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185-294/Domain: Clr/Cls repeat homology <C1R2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: mRNA
Residues: 1-699 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 le: Molecular characterization of a novel serine protease involved in activation rence number: I54763; MUID:94289349; PMID:8018603 ssion: I54763 ssion: I54763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -362/Domain: complement factor H repeat homology <FH1>
432/Domain: complement factor H repeat homology <FH2>
432/Domain: complement factor H repeat homology <FH2>
691/Domain: trypsin homology <FRY>
691/Domain: trypsin homology <FRY>
78,407/Binding site: carbohydrate (Asn) (covalent) #status predicted
91.143-157,153-166,168-181,185-212,242-260,301-349,329-362,367-414,397-432,436-572,
                                                                                                                                                                                                                                               27
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                                                                                                                                                                                                                                                                                         11 VFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
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                                                                                                                                                                                                                                             MFGQIQSPGYPDSYPSDSEVTWNITVPDGFR 57
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  to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                              Similarity
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  EMBL
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  Data
                                                                                                                                                                                                                                                                                                                                                              39.1%;
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  Library, February 1994
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                                                                                                                                                                                                                                                                                                                                 Pred. No. U.U.
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      precursor - human
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Pred. No. 4 7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein-associated
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                                                                     20-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                 .0019;
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in; hydro
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                                                                                                                                                                                                        J. Biol. Cnem. 2007.
A;Title: Type I procollagen
A:Arrance number: A55362;
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
A55362
A;Cross-references: GDB:305468;
A;Map position: 7q21.3-7q22
                                                 A; Gene: GDB: PCOLCE
                                                                       C; Genetics:
                                                                                             A; Cross-references: GB:L33799;
                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-449 < TAK>
                                                                                                                                                                A; Status: not compared with
                                                                                                                                                                                         A; Accession: A55362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-610 < FUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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A; Molecule type: mRNA
A; Residues: 1-1290 <LIA>
A; Cross references: GB:U32681; NID:g975346; PIDN:AAC52248.1;
C; Superfamily: scavenger recentor custoficolists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Li, X.J.; Snyder, S.H.
J. Biol. Chem. 270, 17674-17679, 1995
A;Title: Molecular cloning of Ebnerin, a vc
A;Reference number: A57190; MUID:953535352;
A;Accession: A57190
                                                                                            procollagen I C-proteinase enhancer protein precursor C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text
C;Accession: A55362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F:142-245/Domain: scavenger receptor cysteine-rich domain homology F:289-392/Domain: scavenger receptor cysteine-rich domain homology F:583-689/Domain: C1r/C1s repeat homology <C1R1>F:713-816/Domain: scavenger receptor cysteine-rich domain homology F:838-944/Domain: C1r/C1s repeat homology <C1R2>
                                                R; Takahara, K.; Kessler, E.; Bin
J. Biol. Chem. 269, 26280-26285,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:U32681; NID:g975346; PIDN:ARC52248.1; PID:g975347 C;Superfamily: scavenger receptor cysteine-rich domain homology; Clr/Cls repeat homol C;Superfamily: scavenger receptor cysteine-rich domain homology; at the cysteine rich domain homology #status atypical <SRC F:1-77/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Nov-1995 #sequence_revision 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: U00036; NID: g458996; A; Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: The sequence of C. elegans cosmid R151.
A;Reference number: S44639
A;Accession: T16761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 RLASPGFPGEYANDQERRWTLTAPPGY 40
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                                                                                                                                                                                                                                                                                                       GPVWTSPPFVNYTCGGFLTGLSGQFSSPYYPGSYPNNARCLWNIEVPNNYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68/3; 120/1; 151/1; 307/1;
                                                                          Kessler, E.; Biniaminov, L.; Brusel, M.;
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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51.9%;
COOH-terminal proteinase enhancer MUID:95014462; PMID:7523404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid sequence not shown; not compared with conceptual
                                                                                                                                                                                                                                                                                                                                                  GRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 83.5; DB Pred. No. 0.053;
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2; PMID:7629065
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0.015;
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                                                                                                                                                                                                                                                                                                                                                                                                   17;
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                                                                                                                        #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1290;
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                                                                       Eddy, R.L.;
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                         protein: identification
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                                                                             Jani-Sait, S.;
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conceptual translation

NID: g642907; PIDN: AAA61949.1; PID: g642908

OMIM:600270

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A; Molecule type: protein
A; Residues: 464-705 < AR2>
R; Thielens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.;
R; Thielens, Chem. 265, 14469-14475, 1990
A; Title: Ca(2+) binding properties and Ca(2+)-dependent
A; Reference number: A37820; MUID:90354439; PMID:2387866
A; Accession: A37820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Accession: A29768
A:Molecule type: mRNA
A:Residues: 1-151, 'L', 153-705 <JOU>
A:Residues: 1-151, 'L', 153-705 <JOU>
A:Cross-references: GB:X04701; NID:929538; PIDN:CAA28407.1;
R:Arlaud, G.J.; Willis, A.C.; Gagnon, J.
Biochem, J. 241, 711-720, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. J. 240, 783-787, 1986
A;Title: Cloning and sequencing of full-length cDNA encoding A;Reference number: A29768; MUID:87156625; PMID:3030286
                           A:Molecule type: protein
A:Residues: 18-26;'L',53-160;'XX',252-255 <THI>
R:Pelloux, S: Thielens, N.M.; Hudry-Clergeon, G.;
FEBS Lett. 386, 15-20, 1996
                                                                                                                                                                                                                                                                                                                  A;Title: Complete amino acid sequence of the catalytic chain of human complement A;Reference number: A00916; MUID:83204782; PMID:6303394 A;Accession: A00916
                                                                                                                                                                                                                                                                                                                                                                                            R; Arlaud, G.J.; Gagnon, J.
Biochemistry 22, 1758-1764, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 152-186 <AR3>
A; Note: 152-Leu was also i
R; Arlaud, G.J.; Gagnon, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Title: Identification of erythro-beta-hydroxyasparagine in the EGF-like domain A:Reference number: S02422; MUID:88005128; PMID:2820791 A:Accession: S02422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-705 <LEY>
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F;159-270/Domain: C1r/C1s repeat homology <C1R2>
F;26/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form)
F;29,431/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: Clr/Cls repeat homology
C;Keywords: extracellular protein; glyc
F;1-25/Domain: signal sequence #status
F;26-449/Product: #status predicted <MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Journet, A.; Tosi, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: M14058; NID: g179643; PIDN: AAA51851.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Date: 15-Nov-1984 #sequence_revision 30-Jun-1991 #text_change 03-Jun-2002;Accession: A24170; A29768; A29769; S02422; A00916; A37820; S68830;Leytus, S.P.; Kurachi, K.; Sakariassen, K.S.; Davie, E.W. 1966: 10chemistry 25, 4855-4863, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: protein sidues: 18-166,'X',168-463 <ARL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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aud, G.J.; van Dorsselaer
Lett. 222, 129-134, 1987
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  Identification
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      was also found
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of a cryptic protein kinase CK2 phosphorylation
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                                                                                                                                                                                                                                   Lacroix, M.B.; Gagnon, J.;
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                                                                                                                                                                                 interactions of
                                                                                                                                                                                                                                     Arlaud,
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                                                 Y . ;
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                                              Filhol,
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F;18-463/Product: complement Clr chain A #status experimental <ACH>
F;146-189/Domain: EGF homology <EGFP>
F;193-302/Domain: Clr/Cls repeat homology <CIR2>
F;297-463/Product: Clr gamma fragment #status experimental <GFP>
F;297-463/Product: Clr gamma fragment #status experimental <GFP>
F;309-371/Domain: complement factor H repeat homology <FH1>
F;306-447/Domain: complement Clr chain B #status experimental <BCH>
F;464-705/Product: complement Clr chain B #status experimental <BCH>
F;464-697/Domain: trypsin homology <FRY>
F;1464-697/Domain: trypsin homology <FRY>
F;1-89.146-165,161-174.176-189,193-20,250-268,309-358,338-371,376-429,406-447,451-5
F;125,221,514.581/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;167/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
F;266/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status experime
F;463-464/Cleavage site: Arg-Ile (autolytic) #status experimental
F;502,557,654/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                      C;Superfamily: complement factor H repeat homology F;354-409/Domain: complement factor H repeat homology F;529-586/Domain: complement factor H repeat homology F;707-762/Domain: complement factor H repeat homology F;768-827/Domain: complement factor H repeat homology F;835-892/Domain: complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Shimizu-Nishikawa, K.; Kajiwara, K.; Kimura, M.; Katsuki, M.; Sugaya, E. Brain Res. Mol. Brain Res. 28, 201-210, 1995
A;Title: Cloning and expression of SEZ-6, a brain-specific and seizure-related A;Reference number: I52657; MUID:95240392; PMID:7723619
A;Accession: I52657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: complement subcomponent Clr; Clr/Cls re; C;Seywords: acute phase; beta-hydroxyasparagine; calcif;1-1/Domain: signal sequence #status predicted <SIG>F;17-138/Domain: Clr/Cls repeat homology <Clrl>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seizure-related protein SEZ-6 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:D29763; NID:g693909; PIDN:BAA06167.1;
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A; Residues: 1-977 < RES>
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A; Residues: 133-137;187-211;610-613
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A;Residues: 16-38,68-115;170-236;246-262;265-280;282-284;287-308,315-363;384-394,421-435;7051, M.; Duponchel, C.; Meo, T.; Couture-Tosi, E. J. Mol. Biol. 208, 709-714, 1989
A;Title: Complement genes Clr and Cls feature an intronless serine protease domain close A;Reference number: S05634; MUID:90040704; PMID:2553984
A;Accession: S05634
A;Status: not compared with conceptual translation
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Cross-references: GB:M18767; NID:g179647; PIDN:AAA51853.1; PID:g1796
R:Mackinnon, C.M.; Carter, P.E.; Smyth, S.J.; Dunbar, B.; Fothergill,
Eur. J. Biochem. 169, 547-553, 1197
A;Title: Molecular cloning of cDNA for human complement component Cls.
A:Reference number: S00224; MUID:88082788; PMID:3500856
A;Accession: S00224
A;Molecule type: mRNA
A;Residues: 1-688 <MAC>
A;Cross-references: EMBL:X06596; NID:g29542; PIDN:CAA29817.1; PID:g763
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                                                                                                                                                                                                                                                                                                                                                        A; Accession: S26732
A; Molecule type: pro
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A; Residues: 1-688 < KU
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Residues: 1-688 <TOS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Le: Complete cDNA sequence of human complement C1s erence number: A27381; MUID:88163522; PMID:2831944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 emistry 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.; Duponchel, C.; Meo, 1
istry 26, 8516-8524, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 FGRLASPGFPGEYANDQERRWTLTAPPGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGNLRSPGWPDNYDNDKDCTVTLTAPQNH 3431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3593-3600,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-688 <KUS>
                                                                                                                                                                                                                                                                                                                                                        protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
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Pred. No. 0.
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В

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RESULT

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A; Note: the list of introns may be incomplete
C; Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement
C; Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement
C; Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement
F; 1-15/Domain: signal sequence #status predicted <SIG>
F; 11-127/Domain: Clr/Cls repeat homology <C1R1>
F; 16-688/product: complement subcomponent Cls #status experimental <MAT>
F; 16-437/Product: complement subcomponent Cls #status experimental <MAT>
F; 13-171/Domain: EGF homology <EGF>
F; 13-171/Domain: Clr/Cls repeat homology <C1R2>
F; 17-887/Domain: Clr/Cls repeat homology <C1R2>
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A;Residues: 131-134, 'X',136-146, 'X',148-150;155, 'X',157-162;166-170, 'X',172-174, 'X',1
A;Residues: 131-134, 'X',136-424, 'X',426-431;547-556;592-597;617, 'X',619-627, 'X',629-
R;Thielens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.
J. Biol. Chem. 265, 14469-14475, 1990
A;Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated A;Reference number: A37820; MUID:90354439; PMID:2387866
A;Accession: B37820
                                                                                                                                                                                                             E:438-688/Product: complement subcomponent C1s chain B (light chain) #status experime F:438-675/Domain: trypsin homology <TRY> F:65-83,135-147,143-156,158-171,175-202,234-251,294-341,321-354,359-403,386-421,425-5 F:149/Modified site: erythro-beta-hydroxyasparagine (Asn) (partial) #status experimen F:174,406/Binding site: carbohydrate (Asn) (covalent) #status experimental F:437-430/Cleavage site: Arg-Ile (complement subcomponent C1r) #status experimental F:475-529,632/Active site: His, Asp, Ser #status predicted
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A:Molecule type: protein
A:Residues: 16-25;'X', 203-207 <THI>
R:Thielens, N.M.: Van Oorselaer, A.: Gagnon, J.: Arlaud, G.J.
Biochemistry 29, 3570-3578, 1990
A:Title: Chemical and functional characterization of a fragment of C1s containing
A:Reference number: A32672; MUID:90283368; PMID:2141278
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A:Residues: 16-61:168-219;287-293,'K',295-334;384-445 <S
R:Hess, D.; Schaller, J.; Rickli, E.E.
Biochemistry 30, 2827-2833, 1991
A;Title: Identification of the disulfide bonds of human
A;Reference number: A38407; MUID:91175725; PMID:2007122
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                                                                                                                                                                                                         F;437-438/CIeavage si
F;475,529,632/Active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Carter, P.E.; Dunbar, B.; Fothergill, J.E. Biochem. J. 215, 565-571, 1983
A;Title: The serine proteinase chain of human
A;Reference number: A05140; MUID:84104122; PMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;294-354/Domain: complement factor H repeat homology <FH1>F;359-421/Domain: complement factor H repeat homology <FH2>
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A; Residues: 438-483, 'X', 485-500; 503-534; 542-558; 561-572, 'A', 574-601; 617-623; 626-644; 6
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                                                                                                                 Local
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       7 WPEP-VFGRLASPGFPGEYANDQERRWTLTAPPGY 40
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                                                                                                                 Similarity
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                                                                                                                 31.3%;
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                                                                                                                 Score 74.5; DB Pred. No. 0.33;
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[7]
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0; PMID:3007145
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PMID:6362661
                                                                                                                                               DB 1;
                                                                             13;
                                                                                                                                               Length
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A:Cross-references: EMBL:X57337; NID:g1486405; PIDN:CAA40612.1; PITA A:Experimental source: astroglial cell line D19 C:Superfamily: C1r/C1s repeat homology C:Reywords: duplication; glycoprotein; pyroglutamic acid F:1-24/Domain: signal sequence #status predicted <SIG> -402/Product: procollagen I C-proteinase enhancer protein #status/Domain: C1r/C1s repeat homology <C1R1> -269/Domain: C1r/C1s repeat homology <C1R1> -269/Domain: C1r/C1s repeat homology <C1R2> Modified site: pyrrolidone carboxylic acid (Gln) (in mature fc F728/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Speciles: Mus musculus (house mouse)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 05-Nov-1999
C;Accession: JH0403
R;Lecain, E.; Zelenika, D.; Laine, M.C.; Rhyner, T.; Pessac, B.
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A; Residues: 1-319 <SAT>
A; Cross-references: GB:M27162; NID:g214871; PIDN:AAA49980.1; PID:g214872
C; Superfamily: astacin homology
C; Keywords: zinc
FEBS Lett. 250, 411-415, 1989
A;Title: Complete primary structure of a calcium-dependent serine proteinase
A;Reference number: S05008; MUID:89325606; PMID:2753140
                                                                                                complement subcomponent C 1SBAR.GIF (EC 3.4.21.42) precursor C; Species: Mesocricetus auratus (golden hamster) C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_chan C; Accession: S05008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Neurochem. 56, 2133-2138, 1991
A:Title: Isolation of a novel cDNA corresponding to a transcript A:Reference number: JH0403; MUID:91225708; PMID:2027019
A:Accession: JH0403
                                                         R;Kinoshita, H.; Sakiyama, H.; Tokunaga, K.; FEBS Lett. 250, 411-415, 1989
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A; Residues: 1-402 < LEC>
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Pred. No. 0.17;
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A;Cross-references: EMBL:X16160; NID:g49621; PIDN:CAA34286.1; PID:g49622
A;Note: part of this sequence, including the amino ends of both the heavy and light (C;Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement fact. C;Keywords: beta-hydroxyasparagine; calcium binding; duplication; glycoprotein; hydr:F;1-21/Domain: signal sequence #status predicted <SIG>F;11-13/Domain: cir/C1s repeat homology <C1R1>F;12-444/Product: serine proteinase heavy chain #status experimental <HCH>F;141-177/Domain: EGF homology <EGF>F;181-197/Domain: CIr/C1s repeat homology <C1R2>F;181-293/Domain: CIr/C1s repeat homology <C1R2>F;300-360/Domain: complement factor H repeat homology <FH1>F;354-428/Domain: complement factor H repeat homology <FH2>F;445-682/Domain: trypsin homology <TRY>F;445-682/Domain: trypsin homology <TRY>F;445-682/Domain: trypsin homology <TRY>F;181-133/14-1153/149-162,164-177,181-208,240-257,300-347,327-360,365-410,392-428,432-F;155/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted F:1800,413/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                              tolloid-BMP-1 like protein 1 - California sea hare N;Alternate names: probable metalloprotease TBL-1 C:Species: Aplysia californica (California sea hare) C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #: C;Accession: T31069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; Rasmussen, H.H.; Braul J. Biol. Chem. 273, 5235-5242, 1998
A;Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodi A;Reference number: Z16459; MUID:98148073; PMID:9478979
A;Accession: T08618
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999
                                                          R; Liu, Q.R.; Hattar, S.; Endo, J. Neurosci. 17, 755-764, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; periphe F;1-20/Domain: signal sequence #status predicted <SIG> F;21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted
A; Title: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by A; Reference number: 220965; MUID:98007484; PMID:8987797
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F; 436-467/Domain:
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A; Residues: 1-3623 < M
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A;Status: preliminal, A;Anolecule type: mnMa 
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A;Cross-references: GDB:125203; OMIM:112264
A;Map position: 8p21-8p21
C;Function:
A;Map position: 8p21-8p21
C;Function:
C;Function: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen ty A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen ty C;Superfamily: procollagen C-endopeptidase; astacin homology; C1r/C1s repeat homology; C;Superfamily: procollagen catalyzes homology; C1r/C1s repeat homology; C;Superfamily: procollagen central homology; C1r/C1s repeat homology; C;Superfamily: procollagen central homology; C1r/C1s repeat homology; C;Superfamily: procollagen central homology; C1r/C1s repeat homo
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A;Title: Novel regulators of bone formation: molecular clones A;Reference number: A37278; MUID:89072730; PMID:3201241 A;Accession: A37278 A;Accession: A37278 A;Accession: A37278
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zney, J.M.; Rosen, V.; (
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/Modified site: erythro-beta-hydroxyasparagine (Asn) #status
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A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen t C;Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; C;Keywords: alternative splicing; beta hydroxyasparagine; bone; calcium; duplication; F;1-22/Domain: signal sequence *status predicted <SIG>F;23-823/Product: procollagen C-endopeptidase splice form HIS *status predicted <MAT>F;232-431/Domain: astacin homology <AST>F;330-321/Domain: clr/Cls repeat homology <CIR1>F;325-544/Domain: Clr/Cls repeat homology <CIR2>F;551-587/Domain: Clr/Cls repeat homology <CIR2>F;591-790/Domain: Clr/Cls repeat homology <CIR3>F;738-752/Region: histidine-rich F;738-752/Region: histidine-rich F;91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) *status predicted F;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644 F;213,217,223,272/Binding site: zinc (His, His, His, Tyr) *status predicted F;214/Active site: Glu *status predicte
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A;Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld)
A;Reference number: A58788; MUID:95096114; PMID:7798260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position:
C; Function:
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A;Map position: 8p21-8p21
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A; Residues: 703-823 <TAK>
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A;Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
R;Takahara, K.; Lyons, G.E.; Greenspan, D.S.
J. Biol. Chem. 269, 32572-32578, 1994
                                                                                                                                                                                                                                                                                                                                                                                   F;565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-702, 'EKRPALQPPRGRPHQLKFRYQKRNRTPQ'
A; Cross-references: GB: M22488; NID: g179499; PIDN
A; Cross-references: G-E: Greenspan, D.S. A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen to C;Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cis repeat homology C;Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; F;1-22/Domain: signal sequence #status predicted <SIG> A;Cross-references: GDB:125203; OMIM:112264 A;Map position: 8p21-8p21 C;Function: N;Alternate names: bone morphogenic protein 1, tolloid-like splice form
C;Species: Homo sapiens (man)
C;Date: 28-Mar-1998 #sequence\_revision 09-Apr-1998 #text\_change 16-Jul-1999 A;Cross-references: GB:L35279; C;Genetics: A; Molecule type: mRI A; Residues: 703-986 C; Date: 28-Mar-1998 #sequenc C; Accession: A37278; B58788 A; Gene: GDB: BMP1; BMP-1 A; Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are A; Reference number: A58788; MUID:95096114; PMID:7798260 J. Biol. Chem. 269, 32572-32578, 1994 A; Title: Novel regulators of bone formation: molecular clones and activities A; Reference number: A37278; MUID:89072730; PMID:3201241 R; Wozney, J.M.; Rosen, V.; Co Science 242, 1528-1534, 1988 A; Accession: B58788 A; Accession: A37278 procollagen C-endopeptidase (EC 3.4.24.19) precursor, mRNA <TAK> Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, NID: g619860; RTPQ' <WOZ>
PIDN:AAA51833.1; PIDN: AAC41710.1; tolloid-like PID:g619861 PID:g179500 splice form Σ huma en

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C;Species: Drosophila melanogaster
C;Date: 19-Uul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C;Accession: S58984
R;Finelli, A.L.; Xie, T.; Bossie, C.A.; Blackman, R.K.; Padgett, R.W.
Genetics 141, 271-281, 1995
                                                                                                                                                                                                                                                                                         RESULT
S58984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I49540
    A; Molecule type: mRNA
A; Residues: 1-1464 <FIN>
A; Cross-references: EMBL
                                                                         A;Title: The tolkin gene is a tolloid/BMP-1 homologue that is A;Reference number: S58984; MUID:96042912; PMID:8536976 A;Accession: S58984
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F;860-973/Domain: C1r/C1s repeat homology <C1R5>
F;860-973/Domain: C1r/C1s repeat homology <C1R5>
F;91.142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66
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A; Residues: 1-991 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Embryonic expression of mouse bone morphogenetic A; Reference number: I49540; MUID:94229342; PMID:8174772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Fukagawa, M.; Noboru, ;
Dev. Biol. 163, 175-183,
                                                                                                                                                                                                                                                            development protein tolkin (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)
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Matches
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556-592/Domain: EGF homology <EG1>
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Best Local
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435-544/Domain: Clr/Cls repeat homology <ClR2>
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130-321/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   596-705/Domain: Clr/Cls repeat homology <Clr>412-747/Domain: EGF homology <EG2>
,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted
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13; Conservative
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EMBL: U34777; NID: g1002985; PIDN: AAC47015.1;
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  PID: g1002986
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A;Cross-references: FlyBase:FBgn0004885
C;Superfamily: astacin homology; EGF homology
C;Keywords: hydrolase; metalloproteinase; zinc
F;529-722/Domain: astacin homology <AST>
F;958-993/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                     Biochem. J. 310, 41-48, 1995
A;Title: Bovine gall-bladder mucin contains two distinct A;Reference number: S56744; MUID:95374471; PMID:7646470
A;Accession: S56745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
S56745
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                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
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Search completed: January Job time: 69 secs
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                                                                                                                                                                                                          F;311-417/Domain: scavenger receptor cysteine-rich
                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-504 < NU
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12; Conserv
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9: sp_phage:*
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93	93	100	164	164	164	170	180	183	183	183	183	183	238	238	238	Score	
39.1	39.1	42.0	68.9	68.9	68.9	71.4	75.6	76.9	76.9	76.9	76.9	76.9	100.0	100.0	100.0	Match	% Query
701	212	889	216	185	177	186	678	685	685	367	190	185	185	181	175	Length	
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Q9JJS9	009020	Q9PVY4	Q9QX83	Q9QX88	Q9QX86	Q9QXD4	Q9JJS8	Q91WP0	Q9Z338	Q9QXD2	Q9QXD5	Q9QXA4	Q9UBP3	Q9ULC7	Q9UMV3	ID	
Q9jjs9 rattus norv	_	Q9pvy4 xenopus lae		Q9qx88 rattus norv	Q9qx86 rattus norv		tus	-	Q9z338 mus musculu		•	-	homo	•	Q9umv3 homo sapien	Description	

## ALIGNMENTS

RL	RT	RT	RT	RA	RA	RX	RC	RP	RN	o X	8	8	SO	GN	DE	DE	DŢ	DŢ	ΡŢ	AC	ID	RESULT Q9UMV3
J. Immunol. 162:3481-3490(1999).	structural gene.";	lectin activation pathway of complement are encoded by a single	"Two constituents of the initiation complex of the mannose-binding	Jensenius J.C., Schwaeble W.J.;	Stover C.M., Thiel S., Thelen M., Lynch N.J., Vorup-Jensen T.,	MEDLINE=99192764; PubMed=10092804;	TISSUE-LIVER;	SEQUENCE FROM N.A.	(1)	NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	MASP-2.	MAp19 (19kDa) precursor (Fragment).	Mannose binding lectin-associated serine protease-2 related protein,	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	01-MAY-2000 (TremBLrel. 13, Created)	Q9UMV3;	Q9UMV3 PRELIMINARY; PRT; 175 AA.	RESULT 1 Q9UMV3

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Query Match
Best Local Similarity
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Best Local Similarity
                                                                        SMART; SMOO042; CUB; 1.

SMART; SMOO179; EGF_CA; 1.

SMART; SMOO179; EGF_CA; 1.

PROSITE; PSO01180; CUB; 1.

PROSITE; PSO1186; EGF_2; 1.

PROSITE; PSO1187; EGF_CA; 1.

PROSITE; PSO1187; EGF-Like domain; G.

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PROSITE; PSO1186; EGF_2; 1.
PROSITE; PSO1187; EGF_CA; 1.
Calcium-binding; EGF-like domain;
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InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
Pfam; PF00431; CUB; 1.
                                                             SEQUENCE
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Mammalia;
                                                                                                                                                                                                                                                                                                                                           MEROPS; S01.229;
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SM00179; EGF_CA; 1.
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IPR000859; CUB_domain.
IPR000561; EGF-like.
IPR001881; EGF_Ca.
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                                                             181 AA;
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Score 238; DB 4;
Pred. No. 3.2e-23;
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                                                                                                Glycoprotein;
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matches 0;
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                                                                                                  Protease;
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                    Length 181;
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Q9UBP3;
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O1-MAY-2000 (TEMBLrel. 13, C
01-MAY-2000 (TEMBLrel. 13, L
01-JUN-2002 (TEMBLrel. 21, L
01-JUN-2002 (TEMBLrel. 21, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99262288; PubMed=10330290; Takahashi M., Endo Y., Fujita T., Matsushita M.; Matsushita M.; Takahashi M., Endo Y., Fujita T., Matsushita M.; Matsush
                           PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGE_2; 1.
PROSITE; PS01187; EGF_CA; 1.
                                                                                                                                                                                                                                                                     InterPro;
InterPro;
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"Partial genomic structure of human
(MASP)-2 (from exon 1 to exon 5).";
Submitted (OCT-1999) to the EMBL/Ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99192764: PubMed=10092804;
Stover C.M., Thiel S., Thelen M., Lynch N.J.
Jensenius J.C., Schwaeble W.J.;
"Two constituents of the initiation complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAP19 (19 kDa) precursor (19 kDa) MASP-2 OR SMAP OR MASP2.
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Mannose binding lectin-associated serine protease-2 related protein,
MAP19 (19 kDa) precursor (19 kDa) (MBL-associated protein MAP19).
Calcium-binding; EGF-like domain; Glycoprotein; Lectin; Protease;
                                                                                                                                                                   SMART; SM00042; CUB; 1.
SMART; SM00179; EGF_CA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunol.
                                                                                                                                                                                                                                      PF00431; CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                      P00736;
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                                                                                                                                                                                                                                                       IPRO00152; Asx_hydroxyl.
IPRO00859; CUB_domain.
IPRO00561; EGF-like.
IPRO01881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baek K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yoon J.;
-2 Gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA
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                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990XA4
990XA4;
101-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
MOUSE MAP19 precursor.
MASP2 OR MASP-2/MAP19.
                                                                                                                                                                                                                                                                                                                         Pfam; PF00431; CUB; 1.

SMART; SM00042; CUB; 1.

SMART; SM00179; EGF_CA; 1.

PROSITE; PS00100; ASX_HYDROXYL; UNKNOWN_1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS01187; EGF_CA; 1.

Calcium-binding; EGF-like domain; Glycoprotein; Repeat; SIGNAL 1 15

POTENTIAL.
                  Q9QXD5;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLIND=20054576; PubMed=10586086;

MEDLIND=20054576; PubMed=10586086;

Stover C.M., Thiel S., Lynch N.J., Schwaeble W.J.;

The rat and mouse homologues of MASP-2 and MApl9, components mannan-binding lectin activation pathway of complement.";

J. Immunol. 163:6840-6859(1999).

-1-SIMILARITY: CONTAINS 1 CUB DOMAIN.

EMBL; AJ250369; CAB63701.1;

EMBL; BJ250369; CAB63701.1;

HSSP; P00736; 1APO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1330832; Masp2.
InterPro; IPR000152; Asx.hydroxyl.
InterPro; IPR000559; CUB_domain.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; C
                                                                                   Q9QXD5
                                                                                                                                                                                                                                                                                                                    CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
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                                                                                                                                                                                 1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                TLLGSKWPEPVFGRLVSPGFPEKYADHQDRSWTLTAPPGYR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR
                                                                                                                                                                                                                                                  Similarity
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   binding
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                                                                                                                                                                                                                                                                                                  185 AA;
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                  (TrEMBLrel.
                                                                                                                                                                                                                                  Conservative
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                                                                                   PRELIMINARY;
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                                                    (TrEMBLrel.
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   lectin-associated
                                                                                                                                                                                                                                                                                              185 MW;
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185
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Rodentia;
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78.0%;
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               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                 Pred.
3; Mis
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                                                                                                                                                                                                                               Score 183; DB Pred. No. 4.7e 3; Mismatches
                                                                                                                                                                                                                                                                                                MOUSE MAP19.
; 72E01900D30A18B9 CRC64;
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MANNOSE BINDING LECTIN-ASSOCIATED PROTEASE-2 RELATED PROTEIN, MAP19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73B133D56FB229C2 CRC64;
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serine protease-2
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No. 3.3e-23;
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                                                                                                                                                                                                                                                              Length 185;
                                                                                                                                                                                                                                 Indels
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 precursor.
                                                                                                                                                                                                                                                                                                                                                Signal
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RESULT
Q9QXD2
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Best Local :
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Q9QXD2;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2002
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SMART; SM00042; CUB; 1.
SMART; SM000179; EGF_CA; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01181; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
MGD; MGI:1330832; Masp2.
InterPro; IPR000152; Asx_hydrox; InterPro; IPR000859; CUB_domain
                                                                                                     Stover C.M., Thiel S., Lynch N.J., Schwaeble W.J.;
"The rat and mouse homologues of MASP-2 and MAp19, compone
mannan-binding lectin activation pathway of complement.";
J. Immunol. 163:6848-6859(1999).
-: SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-: SIMILARITY: CONTAINS 2 CUB DOMAINS.
-: SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stover C.M., Thiel S., Lynch N.J., Schwaeble "The rat and mouse homologues of MASP-2 and mannan-binding lectin activation pathway of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-C57BL/6 X CBA;
MEDLINE-20054576; PubMed-10586086;
                                                     EMBL; Y19163; CAB65250.1;
HSSP; P00736; 1APQ.
MEROPS; S01.229; -.
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Immunol. 163:6848-6859(1999).
-!- SIMILARITY: CONTAINS 1 CUB DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                MEDLINE=20054576; PubMed=10586086;
                                                                                                                                                                                                                                                    STRAIN-B6CBAF1/J;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                              MASP2 OR MASP-2
                                                                                                                                                                                                                                                                                                                                                                                                             Mannose binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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[1]
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLLGSKWPEPVFGRLVSPGFPEKYADHQDRSWTLTAPPGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y19160; CAB65247.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                          (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                           lectin-associated serine protease-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 F
21457 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.9%;
78.0%;
                  Asx_hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 183; DB
Pred. No. 4.9e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ω
-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22BC6BA3F906B010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schwaeble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9e-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e W.J.;
MAp19, components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                               components
                                                                                                                                                                                                                                                                                                                       Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                           precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0f
                                                                                                                                                                                               of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9Z338;
01-MAY-1999
01-MAY-1999
                                                                                                                                                                   Pfam;
SMART; SM00032; CCP; 2.
SMART; SM00042; CUB; 2.
SMART; SM00179; EGF_CA;
SMART; SM00020; Tryp_SPc
                                                                                                                                                                                                             InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR0001314; Chymotrypsin.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001254; Ser_protease_
                                                                                                                                                                                                                                                                                                                                                                                                           TRYPSIN FAMILY.
EMBL; AB009459; BAA34674.1;
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Mannose-binding lectin associated serine protease-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00431; CUB; 2.
Pfam; PF00084; sush1; 1.
Pfam; PF00084; sush1; 1.
SMART; SM00032; CCCP; 1.
SMART; SM00032; CCUB; 2.
SMART; SM00042; CUB; 2.
SMART; SM00179; EGF_CA; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01180; CUB; 2.
PROSITE; PS01186; EGF_Z; 1.
PROSITE; PS01187; EGF_CA; 1.
Calcium-binding; EGF-like domain; Glycoprotein; Lectin; Protease;
                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endo Y., Takahashi M., Nakao M.,
Nonaka M., Fujita T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/C; TISSUE=LIVER;
MEDLINE=99008558; PubMed=9794427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MASP2 OR MASP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9Z338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                             PRINTS; PR00722;
                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; S01.229; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004825; InterPro; IPR000436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Two lineages of mannose-binding lectin-associated MASP) in vertebrates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 TLLGSKWPEPVFGRLVSPGFPEKYADHQDRSWTLTAPPGYR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunol. 161:4924-4930(1998).
- SIMILARITY: CONTAINS 2 CUB DOMAINS.
- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                               MGI:1330832; Masp2.
                                                                                             PF00084; sushi; 2.
PF00089; trypsin; 1.
s; PR00722; CHYMOTRYPSIN
                                                                                                                                                                PF00431; CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                           IPR000436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000561;
IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367
367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 F
367
40950 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-like.
EGF_Ca.
Ins/IGF/relax.
Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.9%;
78.0%;
                                                                                                                                                                                         Ser_protease_Try.
Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                    .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 183;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F66FCB29CEAB2B7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saiga H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sekine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Η.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matsushita M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT
Q9JJS8
ID Q9
AC Q9
DT 01
DT 01
DT 01
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Q91WP0
ID Q9
                                                                                                                                 Ωy
                                                                                                            Вb
                                                                                                                                                                                                          Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 32
                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; EGF_2; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00135; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Calcium-binding; EGF-1ike domain; Glycoprote; Protease, Repeat; Serine protease.
SEQUENCE 685 AA; 75490 MW; 4571E1AE0703A;
Q9JJS8
Q9JJS8;
Q1-OCT-2000
Q1-OCT-2000
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                 InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      091WPO:
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Similar to mannan-binding lectin serine protease
                                                                                                                                                                                                        PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS01187; EGF_CA; UNKNOWN_1.
PROSITE; PS00240; TRYPSIN_DOW; 1.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
Hydrolase; Lectin; Protease; Serine protesses
                                                                                                                                                                                                                                                                               PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1. PROSITE; PS01180; CUB; 2.
                                                                                                                                                                                                                                                                                                                 Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                              Pfam; PF00084; sushi; 2.
                                                                                                                                                                                                                                                                                                                                          Pfam; PF00431; CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; S01.229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q91WP0
                                                                                                                                                                                                                                                                                                        SMART; SM00181; EGF;
                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                        [nterPro;
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                                                                                                            16
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                                                                                                                        1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                          TLLGSKWPEPVFGRLVSPGFPEKYADHQDRSWTLTAPPGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLLGSKWPEPVFGRLVSPGFPEKYADHQDRSWTLTAPPGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                         tted (SEP-2001) to the EMBL/GenBank/DDBJ databases BC013893; \mbox{AAH13893.1}; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Conservative
                                                                                                                                                                                                                                                                                                                                                  j IPR000152; Asx_hydroxyl.
j IPR000859; CUB_domain.
j IPR000561; EGF_like.
j IPR001881; EGF_Ca.
j IPR001254; Ser_protease_Try.
j IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa;
                                                                                                                                                          Conservative
                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                      76.9%;
78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.9%;
78.0%;
                                                                                                                                                                    Score 183; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                         erine protease.
F56A6D522BC7099D CRC64;
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                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          685
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                                                                                                                                                                      DB 11;
.2e-15;
                                                 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
otease 2.
                                                                                                                                                          6
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                                                                                                                                                                              Length
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                  685;
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                                                                                                                                                         0;
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) (TrEMBLrel. ) (TrEMBLrel. ? (TrEMBLrel.

15, 15, 21,

Created)
Last sequence update)
Last annotation update)

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RESULTION OF THE PRODUCT OF THE PROD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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SMART; SM00032; CCP; 2.
SMART; SM00032; CCB; 2.
SMART; SM00042; EGF_CA; 1.
SMART; SM000420; Tryp_SPc; 1.
SMART; SM00020010; ASX_HYDROXYL; UNKN PROSITE; PS001180; CUB; 2.
PROSITE; PS01186; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS0135; TRYPSIN_DOM; 1.
PROSITE; PS0135; TRYPSIN_SER; 1.
Calcium-binding; EGF-11ke domain; G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR000152; Asx_hydroxyl.
InterPro: IPR001314; Chymotrypsin.
InterPro: IPR000859; CUB_domain.
InterPro: IPR000561; EGF-like.
InterPro: IPR001861; EGF_Ca.
InterPro: IPR001254; Ser_protease_Ti
InterPro: IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                    01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteases: Effects of naturally occuring. Biol. Chem. 275:30962-30969(2000).
-i- SIMILARITY: CONTAINS 2 CUB DOMAINS.
-i- SIMILARITY: BELONGS TO PEPTIDASE FA
                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ277747; CAB90832.1; HSSP; P00763; 1DPO.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                     MASP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20469449; PubMed=10913141;
    SEQUENCE
                                                                                                       Rattus norvegicus (Rat).
                                                                                                                               MASP-2.
                                                                                                                                                                                                                                                        09QXD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ry Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mannose-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                             TLLGSKWPEPVFGRLVSPGFPEKYGNHQDRSWTLTAPPGFR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00431; CUB; 2.
PF00084; sushi; 2.
PF00089; trypsin; 1.
                                                                                                                                                 protein
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    FROM N.A
                                                                                                                                                                  0 (TrEMBLrel.
0 (TrEMBLrel.
2 (TrEMBLrel.
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                                                                                                                                                 precursor.
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                                                             Chordata;
Rodentia;
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75
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13,
21,
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Pred. No. 5.3e
3; Mismatches
                                                                                                                                                                  Last sequence update)
Last annotation update)
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Sciurognathi;
                                                             Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16680E4A9ADCCC05 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Hydrolase;
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                                                             Vertebrata;
thi; Muridae;
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5.3e-15;
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; Murinae; Rattus.
                                                                                 Euteleostomi;
                                                               Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNOWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                             Rattus
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RESULT
Q9QX86
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Best Local Similarity
Matches 30; Conserv
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090x86;
01-MAY-2000
01-MAY-2000
01-JUN-2002
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SMART; SMO0042; CUB; 1.

SMART; SMO0179; EGF_CA; 1.

PROSITE; PS00100; ASX_HYDROXYL; UNKNOWN_1.

PROSITE; PS01180; CUB; 1.

PROSITE; PS01180; EGF_Z; 1.

PROSITE; PS01187; EGF_CA; 1.

Calcium-binding; EGF-1ke domain; Glycoprotein; Repeat;

Calcium-binding; EGF-1ke domain; Glycoprotein; Repeat;

STGNAL 1.
                                          NON_TER
                                                                           SMART; SM00042; CUB; 1.

SMART; SM00179; EGF_CA; 1.

PROSITE; PS00100; ASX_HYDROXYL; UNKNOWN_1.

PROSITE; PS01186; CUB; 1.

PROSITE; PS01186; EGF_CA; 1.

Calcium-binding; EGF-like domain; Glycoprocations of the control of the contr
                                                                                                                                                                                                                                 InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR001881; EGF_Ca.
Pfam; PF00431; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                 "The rat and mouse homologues of MASP-2 and MApl9, comp mannan-binding lectin activation pathway of complement. J. Immunol. 163:6848-6859(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-FISHER 344;
MEDLINE-20054576; Pubmed-10586086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stover C.M., Thiel S., Lynch N.J., Schwaeble W.J.; "The rat and mouse homologues of MASP-2 and MAp19, mannan-binding lectin activation pathway of complem J. Immunol. 163:6848-6859(1999).
                                                                                                                                                                                                                                                                                                                                            EMBL; Y18570; CAB65387.1; HSSP; P00736; 1APQ.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y19161; CAB65248.1; -. HSSP; P00736; 1APQ.
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    SEQUENCE
                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
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IPRO00859; CUB_domain.
IPRO00561; EGF-like.
IPR001881; EGF_Ca.
    177
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(TrEMBLrel. 13, Last seq
(TrEMBLrel. 21, Last ann
in precursor (Fragment).
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                      <sub>∞</sub> ^
  ΑĄ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s (Rat).
Da; Chordata;
ia; Rodentia;
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73.2%;
  20113
  Μ¥.
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Last annotation updat
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Pred. No. 2
POTENTIAL.
92F3CDCA5A1AD489 CRC64;
                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30878EACB604C374 CRC64;
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Mismatches
                                                                                    Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177
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                                                                                 Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  components ment.";
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                                                                               Signal.
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RESULT
Q9QX88
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Best Loc
Matches
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SMART; SM00142; CUB; 1.
SMART; SM00179; EGF_CA; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF_C; 1.
PROSITE; PS01186; EGF_C; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
SIGNAL

15
POTENTIAL.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09QX88;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                          Q9QX83 PRELIMINARY; PRT; 216 AA. Q9QX83; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) MASP-2 precursor (Fragment).
                                                                                                                                                                                                                  SIGNAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20054576; PubMed=10586086; Stover C.M., Thiel S., Lynch N.J., Schwaeble W.J.; "The rat and mouse homologues of MASP-2 and MAp19, components mannan-binding lectin activation pathway of complement."; J. Immunol. 163:6848-6859(1999).
               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                    HSSP: P00736; lAPQ.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
                                           Rattus norvegicus (Rat).
                                                    MASP-2
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-FISHER 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Sukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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 SEQUÉNCE
                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                   lammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                y Match
                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                 16
                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                TLLGSKWPEPVFGRLVSLAFPEKYGNHQDRSWTLTAPPGFR
                                                                                                                                                                                                                                                                                                                                             Y18568; CAB65385.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                 ch 68.9%; Similarity 70.7%; 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
 N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor
                          Chordata;
Rodentia;
                                                                                                                                                                                                                  21010 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.9%;
70.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13,
13,
21,
                                                                                                                                                                                                                                                                                                                                                        CUB DOMAIN
                                                                                                                                                                                ; Score 164; DB
; Pred. No. 1.4e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ω
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                         Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                  AF22111364C5140C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164;
No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185
                        Vertebrata; Euteleostomi;
איייילאם: Murinae; Rattus
                                                                                                                                                                                        DB 11;
1.4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
L.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9;
                                                                                                                                                56
                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                ō,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                Gaps
                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
В
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Query Match
Best Local S
Matches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0277; INSULINB.
SMART; SM00042; CUB; 1.
SMART; SM00104; EGF CA; 1.
PROSITE; PS00100: ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01180; EGF_CA; 1.
PROSITE; PS01180; EGF_CA; 1.
Calcium-binding; EGF-like domain; Glycoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9PVY4; PRELIMINARY; O9PVY4; 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
InterPro;
                                                                                                             EMBL; AB009072; BAA
HSSP; P00763; 1DPO.
MEROPS; S01.229; -.
                                                                                                                                                                                                                                                       Endo Y., Takahashi M., Nakao M.,
Nonaka M., Fujita T.;
"Two lineages of mannose-binding
                                                                                                                                                                                                                                                                                                                                                                                                                 Mannose-Diluziny Faccos.

Xenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Mannose-binding protein-associated serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stover C.M., Thiel S., Lynch N.J., Schwaeble W.J.;
"The rat and mouse homologues of MASP-2 and Map19, compone
mannan-binding lectin activation pathway of complement.";
J. Immunol. 163:6848-6859(1999).
i- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
i- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                  J. Immunol. 161:4924-4930(1998).
-!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y18573; CAB65390.1; HSSP; P00736; 1APQ.
                                     InterPro;
                                                                                                                                                                                                                                                                                                              MEDLINE=99008558; PubMed=9794427;
                                                                                                                                                                                                                                                                                                                                 TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00431; CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                      InterPro;
                                                       InterPro;
                                                                          InterPro;
                                                                                           InterPro;
                                                                                                                                                                                                                                        (MASP) in vertebrates."
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR004825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20054576; PubMed=10586086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=FISHER 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                   TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLLGSKWPEPVFGRLVSLAFPEKYGNHQDRSWTLTAPPGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
                  p; IPR000152; Asx_hydroxyl.
p; IPR001314; Chymotrypsin.
p; IPR001359; CUB_domain.
p; IPR000561; EGF-like.
p; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000152; Asx_hydroxyl.
IPR000859; CUB_domain.
IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
216
216 A
     IPR001254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                  BAA86865.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
>216
216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24359 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.9%;
70.7%;
Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ins/IGF/relax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF_Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 164;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nain; Glycoprotein;
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A57781AA99B8390C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                          Saiga H.,
                                                                                                                                                                                                                                                          lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                889
                                                                                                                                                                                                                                                          -associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                            Sekine H.,
                                                                                                                                                                                      S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56
                                                                                                                                                                                      ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  components of the
                                                                                                                                                                                                                                                          serine
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                                                                                                                                                                                      KNOWN
                                                                                                                                                                                                                                                                                              Matsushita M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216;
                                                                                                                                                                                                                                                          protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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IPR000436; Sushi\_SCR\_CCP

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RESULT
009020
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                                                            RRA PROCCOCE DIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF00008; EGF; 1.

R Pfam: PF00008; EGF; 1.

R Pfam: PF00008; EGF; 1.

R Pfam: PF000084; sushi; 2.

R Pfam: PF000084; sushi; 2.

R Pfam: PF000092; trypsin; 1.

R PRINTS; PR001722; CHYMOTRYPSIN.

SMART; SM000032; CGF; 2.

SMART; SM000032; CGF; 2.

SMART; SM000020; Tryp_SPC; 1.

SMART; SM00010; ASX_HYDROXYL; UNKNOWN_1.

SMART; SM001010; ASX_HYDROXYL; UNKNOWN_1.

SMART; PS01180; CUB; 2.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01187; EGF_2; 1.

R PROSITE; PS010135; TRYPSIN_DOM; 1.

R PROSITE; PS010135; TRYPSIN_SER; 1.

R PROSITE; PS010136; TRYPSIN_SER; 1.

R PROSITE; SETINE PIOTEASE.

REQUENCE 688 AA; 77513 MW; 180DD559EF8B6573 CRO
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
    Matches
                                                                                               MEROPS; S01.198; -.

InterPro; IPR000152; Asx_hydroxyl.

InterPro; IPR000859; CUB_domain.

InterPro; IPR000851; EGF-like.

InterPro; IPR001881; EGF_Ca.

Pfam; PF00431; CUB; 2.

SMART; SM00042; CUB; 1.

SMART; SM00042; CUB; 1.

SMART; SM00179; EGF_CA; 1.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01180; EGF_CA; 1.

Calcium-binding; EGF-like domain; Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             009020;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Ra-reactive factor serine protease pl00 (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                             ab. Invest. 0:0-0(1997).

- SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL: AF004661; AAB65832.1; -.
HSSP: P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                  Knittel T., Fellmer P., Neubauer
Ramadori G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             009020
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                                                                    "The complement
                                                                                                                                                                                                                                                                                                                                                                     nd is induced
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                                                                                                                                                                                                                                                                                                                                                       ivo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 VFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 LFGRISSPGFPKPYSNDLTMNWNIKVPEGYR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 51.0 es 16; Conservative
                                                           212
212 AA;
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                   t activating by IL-6 in v
                                                           212
24377 MW;
               39.1%;
45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.0%;
51.6%;
                                                                                                                                                                                                                                                                                                                                                                     vitro and
 : Score 93; DB
: Pred. No. 0.00
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 100; DB Pred. No. 0.00 5; Mismatches
                                                         1BB2F52BF0D30A7E
                                                                                                                                                            UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                              ×.
                                                                                                  Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                  p100 is
                                                                                                                                                                                                                                                                                                                                                                                                              Kawakami M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212
                              DB 11;
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).00014;
               .00029;
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                           Length 212;
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                                                           CRC64;
                                                                                                     Protease;
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 Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Grundmann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                   phase
                                                                                                                                                                                                                                                                                                                                                                                  γď
                                                                                                                                                                                                                                                                                                                                                                                 hepatocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease;
                                                                                                                                                                                                                                                                                                                                                                                                              Α.,
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 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus.
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Gaps
                                                                                                                                                                                                                                                                                                                                                                     'n
0;
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RESULT 16
Q9JJS9
  Вb
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                                                                           Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                       InterPro; IPRO00152; Asx_hydroxyl.
InterPro; IPRO00152; Asx_hydroxyl.
InterPro; IPRO00153; CUB_domain.
InterPro; IPRO001881; EGF_Ca.
InterPro; IPRO001881; EGF_Ca.
InterPro; IPRO001881; EGF_Ca.
InterPro; IPRO001881; EGF_Ca.
InterPro; IPRO001254; Sushi_SCR_CCP.
InterPro; IPRO00436; Sushi_SCR_CCP.
InterPro; IPRO00436; Sushi_SCR_CCP.
InterPro; IPRO00431; CUB; 2.
InterPro; IPRO0089; trypsin; 1.
InterPro; IPRO0089; trypsin; 1.
InterPro; IPRO0089; trypsin; 1.
InterPro; IPRO0089; CCP; 2.
InterPro; IPRO00132; CCP; 2.
InterPro; IPRO00132; CCP; 2.
INTERPRO00132; CCP; 2.
INTERPRO00132; CCP; 2.
INTERPROVED SAX_HYDROXYL; UNKNOWN_1.
INTERPROSITE; PS001186; EGF_CA; 1.
INTERPROSITE; PS01186; EGF_CA; 1.
INTERPROSITE; PS01187; EGF_CA; 1.
INTERPROSITE; EGF_CA; 1.

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Q9JJS9;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Mannose-binding protein associated serine protease-1
                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ277423; CAB89695.1; HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MASP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; S01.198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20469449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                              Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
  29
                     11 VFGRLASPGFPGEYANDQERRWTLTAPPGYR 41 : | | : | | : | | : | 4 | : |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MFGQIQSPGYPDSYPSDSEVTWNITVPEGFR
MFGQIQSPGYPDSYPSDSEVTWNITVPEGFR 59
                                                                             l Similarity 45.:
14; Conservative
                                                                                                                                                                                                                                                                Serine
                                                                                                                                                           701
                                                                                                                                                                                                     <1
22
                                                                                                                                                           AA;
                                                                                                                                                                                                                                                            protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10913141;
                                                                                                                                                                                                   21
701
                                                                                            39.1%;
                                                                                                                                                             79663
                                                                                                                                                             MW.
                                                                         ; Score 93; DB; Pred. No. 0.00
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                                                                                                                                                                              MANNOSE-BINDING PROTEIN ASSOCIATED PROTEASE-1.
                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                           B5CFD619D63CE3DD CRC64;
                                                                                                                                                                                                                                                                                 Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
                                                                                                DB 11;
0.0012;
                                                                                                                   Length 701
                                                                                                                                                                                                                                                                                 Hydrolase;
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursor
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RESULT

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QQ AC 
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-JUN-2002 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MBL-associated serine protease-3.
MASP1 OR MASP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Complement factor MASP-3.
Homo sapiens 'ummar'
                                                                                                                                                                                               "An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS01187; EGF_CA; UNKNOWN_1.
PROSITE; PS01240; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
                                                                                                                                                                                                                  STRAIN-BALB/C; TISSUE=LIVER; Takahashi M., Miura S., Ishii N., Endo Y., Matsushita M., Fujita T.,
                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                      MEROPS; S01.132; -.
MGD; MGI:88492; Masp1.
                                                                                                    Submitted (OCT-2000) to the EMBL; AB049755; BAB69688.1;
                                                                                                                                                                  "An essecial role of MBL-associated serine activation of complement by lectin pathway.
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00431; CUB; 2.
Pfam; PF00084; sushi; 2.
Pfam; PF00089; trypsin; 1.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF284421; AAK84071.1;
nterPro; IPR000152; Asx.hydroxyl.
nterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001244; Ser_protease_Try.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding lectin complement activation Immunity 15:127-135(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dahl M.R., Thiel S., Matsushita M., Fujita T., Willis / Christensen T., Vorup-Jensen T., Jensenius J.C.;
"Masp-3 and its association with distinct complexes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=21378425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q96RS4
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ### HISTORYPEST | HISTORYPEST 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
      IPR000152; Asx_hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine protease.
728 AA; 81860 N
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45.2%;
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                                                                                                                                     EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 93; DB
Pred. No. 0.00
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09B5297A6C14283A CRC64;
                                                                                                                                                                                                                                                             Sugamura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0012;
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                                                                                                                                                                               protease-1 and
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                                                                                                                                                                                                                                                             Shuichi
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Q9UC48
         밁
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Best Local :
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Best Local :
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                                                                                                                                                                                                                                                                                                Q9UC48 PRELIMINAKY;
Q9UC48;
01-MAY-2000 (TrEMBLrel. 13, Cr
01-MAY-2000 (TrEMBLrel. 14, Lr
01-JUN-2000 (TrEMBLrel. 14, Lr
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Q8TD25;
01-JUN-2002
01-JUN-2002
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Pfam; PF00084; sushi; 2.
Pfam; PF00089; trypsin; 1.
SMART; SM00181; EGF; 1.
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
MEDLINE=96212543; PubMed=8618346; Rasmussen H.H., Orntoft T.F., Wolf H., "Towards a comprehensive database of p
                                                                                                                                                                                                                                                                      vi-mar-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation updat 18.5 kDa tumor marker protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY038048; AAK71497.1; -. SEQUENCE 996 AA; 107585 MW; E8012D30969D925E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE: PS01180; CUB; 2.
PROSITE: PS01186; EGF_2; UNKNOWN_1.
PROSITE: PS01187; EGF_CA; UNKNOWN_1.
PROSITE: PS0240; TRYPSIN_DOM; 1.
PROSITE: PS0240; TRYPSIN_SER; UNKNOWN_1.
PROSITE: PS00135; TRYPSIN_SER; UNKNOWN_1.
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SEQUENCE
                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                             Homo sapiens (Human).
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SO SEQUENCE 16 AA. 1751 MM: 289540537AlB4400 CRC64;

Query Match 36.6%; Score 87; DB-4; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
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Search completed; January 11, 2003, 10:51:43

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ALIGNMENTS

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PROSITE; PS01180; CUB; 2.

PROSITE; PS01186; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Complement pathway: Serine pro-
Glycoprotein; Sushi; Repeat; Signal; EGF-
SIGNAL 1.

15

POTENTIAL.
            DOMAIN
ACT_SITE
                                                                      DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
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                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00722; CHYMOTRYPSIN
SMART; SM00032; CCP; 2.
MART; SM00042; CUB; 2.
MART; SM000179; EGF_CA; 1.
MART; SM00020; Tryp_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-2000) to the EMBL/CenBank/DDBJ databases.
                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ntities requires a license agreement (Son send an email to license@isb-sib.ch).
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X98400; CAA67050.1; -. 

Y18287; CAB50735.1; -. 

Y18286; CAB50733.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00089; trypsin; 1. PF00431; CUB; 2.
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AF321558; AAG50274.1; JOINED.
AF321559; AAG50274.1; JOINED.
AF321560; AAG50274.1; JOINED.
AF321561; AAG50274.1; JOINED.
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Chymotrypsin.
EGF-like.
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Sushi_SCR_CCP
; 2.
SUSHI 2.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                   SUSHI
                                                                                                                                      CUB
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                                                                                                                                                               EGF-LIKE,
                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                  CALCIUM-BINDING
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RESULT
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Best Local
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P48740; 095570; Q9UF09;
01-FEB-1996 (Rel. 33, Created)
15-GCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Complement-activating component of Ra-reactive factor precursor
(EC 3.4.21.-) (Ra-reactive factor serine protease p100) (RaRF)
(Mannan-binding lectin serine protease 1) (Mannose-binding protease)
associated serine protease) (MASP-1).
MASP1 OR CRARF OR CRARF1 OR PRSS5.
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                    MEDLINE=97079701; PubMed=8921412; Endo Y., Sato T., Matsushita M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
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MOD_RES
"Exon structure of the gene encoding the human mannose-binding protein-associated serine protease light chain: comparison with
                                                                             Sato T., Endo Y., Matsushita M., Fujita T.; "Molecular characterization of a novel serine protease involved activation of the complement system by mannose-binding protein." Int. Immunol. 6:665-669(1994).
                                                                                                                                                                  Takada F., Takayama Y., Hatsuse H., Kawakami M.;
"A new member of the C1s family of complement proteins found bactericidal factor, Ra-reactive factor, in human serum.";
Biochem. Biophys. Res. Commun. 196:1003-1009(1993).
                                                        SEQUENCE FROM
                                                                                                                       MEDLINE=94289349; PubMed=8018603;
                                                                                                                                   TISSUE=Fetal
                                                                                                                                                                                                                           TISSUE=Liver;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
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                                              TISSUE⇒Pl
                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                    iver;
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Primates;
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D -> Y (IN REF. 4).
L -> LCS (IN REF. 4).
G -> E (IN REF. 4).
G -> E (IN REF. 4).
MISSING (IN REF. 3).
L -> LIL (IN REF. 3).
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Pred. No. 1.8e-20;
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Catarrhini;
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                     Fujita T.;
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RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                     Vertebrata; Euteleostomi; Hominidae; Homo.
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Takayama Y., Takada F., Nowatari M., Kawakami M., Matsu-ura N
"Gene structure of the P100 serine-protease component of the reactive factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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Int. Immunol. 8:1355-1358(1996).
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Immunol. 36:50-514(1999).

Immunol. 36:50-514(1999).

Immunol. 36:50-514(1999).

RAPE FUNCTION: COMPONENT OF THE BACTERICIDAL RA-REACTIVE EACTOR RARE FUNCTION: COMPONENT OF TRIGGERS THE ACTIVATION OF COMPLEMENT CASCADE BY ACTIVATING THE C4 AND C2 COMPONENTS. IT ACTIVATES THE C4 CAMPONENT BY CLEAVING THE ALPH C2 COMPONENT BY CLEAVING THE ALPH C2 COMPONENT BY CLEAVING THE ALPH C3 COMPONENT BY CLEAVING THE ALPH C4 AND C5 CAMPONENT CRARE IS AN HETERODIMER OF A COMPLEMENT -ACTIVATING COMPONENT. CRARE IS AN HETERODIMER OF A HEAVY (P70) AND A LIGHT CHAIN (P29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LINKED BY A DISULFIDE BOND.

DOMAIN: CRARF HAS A MODULE ORGANIZATION SIMILAR
SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                          L: D61693: BAA34864.1; JOINED.
L: D61694; BAA34864.1; JOINED.
L: AB007617; BAA89206.1; JOINED.
L: AB007602; BAA89206.1; JOINED.
L: AB007603; BAA89206.1; JOINED.
L: AB007604; BAA89206.1; JOINED.
L: AB007605; BAA89206.1; JOINED.
L: AB007606; BAA89206.1; JOINED.
L: AB007606; BAA89206.1; JOINED.
L: AB007609; BAA89206.1; JOINED.
L: AB007610; BAA89206.1; JOINED.
L: AB007611; BAA89206.1; JOINED.
L: AB007612; BAA89206.1; JOINED.
L: AB007613; BAA89206.1; JOINED.
L: AB007614; BAA89206.1; JOINED.
L: AB0076156; BAA89206.1; JOINED.
L: AB0076166; BAA89206.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L; AB010822; BAA34864 1; JOINED.
L; AB010813; BAA34864 1; JOINED.
L; AB010814; BAA34864 1; JOINED.
L; AB010815; BAA34864 1; JOINED.
L; AB010816; BAA34864 1; JOINED.
L; AB010817; BAA34864 1; JOINED.
L; AB010819; BAA34864 1; JOINED.
L; AB010819; BAA34864 1; JOINED.
L; AB010820; BAA34864 1; JOINED.
L; AB010821; BAA34864 1; JOINED.
L; AB010821; BAA34864 1; JOINED.
L; D61692; BAB34864 1; JOINED.
L; D61692
                                                                                                                                                                                                                                                  AB007616;
P00736; 1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D17525; BAA04477.1; D28593; BAA05928.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D61695;
                                                                                                                                                            P00736; 1APQ.
; S01.198; -
HGNC:6901; MASP1.
ipr000152; Asx_hydroxyl.
ipr000859; CUB_domain.
ipr001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAA3486.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ormatics Institute. There are no rest
institutions as long as its content
attement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ТО
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11 VFGRLASPGFPGEYANDQERRWTLTAPPGYR 41 MFGQIQSPGYPDSYPSDSEVTWNITVPDGFR

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Matches
         Query Match
Best Local
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PROSITE; PS01180; CUB; 2.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50240; TRYPSIN_HIS; 1.
                                                                                                                                                                         DISULFID DISULFID DISULFID
                                           CARBOHYD
CONFLICT
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DISULFID
DISULFID
DISULFID
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SMART;
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DOMAIN
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Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00089; trypsin; 1.
Pfam; PF00431; CUB; 2.
PRINTS; PR00722; CHYMOTRYPSIN..
                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                     SEQUENCE
                                                                                                                            CARBOHYD
                                                                                                                                      CARBOHYD
                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SM00032; CCP; 2.
; SM00042; CUB; 2.
; SM00181; EGF; 1.
; SM00179; EGF_CA; 1.
; SM00020; Tryp_SPC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00084; sushi;
Similarity 45.:
L4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000561;
IPR001881;
IPR001254;
IPR000436;
                                                                                                                                                                                                                                                                                                                                                                                                                     Complement pathway;
                                                                                                                                                                                                                                                                                                                                                                                                             Sushi;
                                    ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                           699
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EGF_Ca.
                                   79258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ser_protease_fry.
Sushi_SCR_CCP.
         39.1%;
45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                            Repeat;
                                    Ψ¥;
                                         N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
O-E (IN REF. 1).
A-> G (IN REF. 1).
K-> E (IN REF. 2).
C-> K (IN REF. 3).
C-> K (IN REF. 3).
D-> V (IN REF. 1).
         Pred.
                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                     SUSHI 1.
SUSHI 2.
                                                                                                                                                                                                                                                                                                                                                                                                    Signal; E
                  Score 93;
                                                                                                                                                                                                                                                                       CHARGE RELAY SYSTEM (BY SII
CHARGE RELAY SYSTEM (BY SII
CHARGE RELAY SYSTEM (BY SII
HYDROXYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                           CUB 1. EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                               RA-REACTIVE FACTOR.
70 KDA CHAIN OF P100
29 KDA CHAIN OF P100
                                                                                                                                                                                                                                                                                                            SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENT-ACTIVATING COMPONENT
                                                                                                                                                       POTENTIAL
                                                                                                                                                               POTENTIAL
                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                         INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                           Serine protease; Proteasin; ignal; EGF-like domain;
 Mismatches
       No.
                                                                                                         (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
IN REF. 1 AND
        DB 1;
).0016;
                                                                                                                                                                        (POTENTIAL).
10;
               Length 699,
                                                                                                                                                                                                                                                                                                                                                                                                                   Protease;
                                   CRC64;
                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                (P70).
(P29).
 Indels
                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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 0
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Gaps
0
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RESULT

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CRAR_MOUSE
                                                                     MGD; MGI:88492; Maspl.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000153; Ctl_domain.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001284; Ser_protease_T.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                     his SWISS-PROT entry is copyright. It is produced through a collaboration etween the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformaticy Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOCHEM. BIOPHYS. Res. COMMUN. 190:681-687(1993).

BIOCHEM. BIOPHYS. Res. COMMUN. 190:681-687(1993).

"HICH SPECIFICALLY BINDS TO RA AND R2 POLYSACCHARIDES EXPRESSED E CERTAIN ENTEROBACTERIA. IT TRIGGERS THE ACTIVATION OF COMPLEMENT CASCADE BY ACTIVATING THE C4 AND C2 COMPONENTS. IT ACTIVATES THE C4 COMPONENT BY CLEAVING THE ALPHA-CHAIN OF C4.

"I SUBUNIT: RARE CONSISTS OF A COMPLEMENT-ACTIVATING COMPONENT (CRARF) AND A POLYSACCHARIDE-BINDING (MANNOSE-BINDING) COMPONENT. CRARF IS AN HETERODIMER OF A HEAVY (P70) AND A LIGH CHAIN (29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P98064;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Complement-activating component of Ra-reactive factor precursor (EC 3.4.21.-) (Ra-reactive factor serine protease p100) (RaRF)
(Mannac, Last)
                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tand Cis."; Takada F., Takahashi A., Ka
TA 100-kDa protein in the C4-activating
factor is a new serine protease having m
                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94179811; PubMed=012
            PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the complement-dependent bactericidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 465-704 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                   MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Presence of a serine protease in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takahashi A., Takayama Y., Hatsuse H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93176166; PubMed=8439319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MASP1 OR CRARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRAR_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol. 152:2308-2316(1994).
                           PF00089; trypsin; 1. PF00431; CUB; 2.
                                                         PF00084; sushi;
                                                                                                                                                                                                                P00736;
                                                                                                                                                                                                                                  D16492; BAA03944.1;
SM00032;
                                                                                                                                                                                                  S01.198;
              PR00722;
                                                                                                                                                                                                                IAPQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver
CCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
            CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND PARTIAL SEQUENCE.
                                                         Ser_protease_Try.
Sushi_SCR_CCP.
; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takahashi A., Kawakami M.;
                                                                                                                                                                                                                                  .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        having module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL
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dal factor, RaRF, in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawakami M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       component of Ra-reactive
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RESULT 4
TOH2_CAEEL
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                                                                                                                                                                                                                        Query Match
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SMART; SM00179; EGF_CA; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00100; ASX_HYDROXYL; 1

PROSITE; PS01180; CUB; 2.

PROSITE; PS01187; EGF_2; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.

PROSITE; PS00134; TRYPSIN_DOM; 1.

PROSITE; PS00135; TRYPSIN_HSER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
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CARBOHYD
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; SIGNAL
Submitted (FEB-1994) to the
        Fulton L.
               STRAIN=Bristol N2;
                         SEQUENCE FROM N.A
                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
                                                                                                                                                                                      11 VFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                 Local
                                                                                                                                                                      32 MFGQIQSPGYPDSYPSDSEVTWNITVPEGFR
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complement
                                                                                                                                                                                                                                          704
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sushi;
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704
1143
1187
302
308
438
438
438
495
704
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1557
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164
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                                                                                                                                                                                                                39.1%;
45.2%;
                                                                                                                                                                                                                                       79895 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat;
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InterPro; IPR001506; Astacin.

InterPro; IPR000859; CUB_domain.

InterPro; IPR000861; EGF-like.

InterPro; IPR000864; TSP1.

InterPro; IPR000130; Zn_MTpeptdse.

Pfam; PF00090; tsp_1; 1.

Pfam; PF00401; CUB; 1.

Pfam; PF01400; Astacin; 1.

Pfam; PF01400; Astacin; 1.

PROMATE; SM00001; EGF_like; 1.

SMART; SM00001; EGF_like; 1.

SMART; SM00235; ZnMC; 1.

PROSTITE; PS01180; CUB; 1.

PROSTITE; PS01180; CUB; 1.
                        CIR_HUMAN STANDARD; PR P00736; 21_JUL-1986 (Rel. 01, Created) 01-AUG-1988 (Rel. 08, Last seque 15-JUN-2002 (Rel. 41, Last annot Complement C1r component precurs C1R.
                                                                                                                                                                                                                                               CARBOHYD
SEQUENCE
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
-!- SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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REVISIONS.
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PROSITE; PS00142; ZINC_PROTEASE; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.
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 Eukaryota;
            Homo sapiens (Human)
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Biochemistry 37:1204-1214(1998).
-i- FUNCTION: C1R B CHAIN IS A SERINE PROTEASE
AND C1S TO FORM C1, THE FIRST COMPONENT OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 133-137; 187-211 AND 609-613, AND MEDLINE-96221263; PubMed-8635594; PubMed-863559459; PubMed-86355969; PubMed-86355969; PubMed-86355969; PubMed-86355969; PubMed-8
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Biochemistry 22:1758-1764(1983).
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Arlaud G.J., Willis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Identification of a cryptic protein kinase CK2 phosphorylation site in human complement protease Clr, and its use to probe intramolecula
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ween the Swiss Institute of Bioinformatics
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                                                                                                         SWISS-PROT entry is copyright. It is produced through
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)5128; PubMed=2820791;
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                                                                                                                           DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                    PROSITE;
PROSITE;
PROSITE;
                             SEQUENCE
                                                                                                                                                                            ACT_SITE
                                                                                                                                                                                           ACT_SITE
                                                                                                                                                                                                                                                                                                       PROSITE;
                                           DISULFID
                                                   DISULFID
                                                          DISULFID
                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                        Complement pathway;
                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:1246; ClR.
                                                                                                                                                        CARBOHYD
                                                                                                                                                            ARBOHYD
                                                                                                                                                                                                                                                                                 Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A24170; C1HURB
                                                                                                                                                                                                                                                                                                                                                                                           PF00089; trypsin; 1. PF00431; CUB; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IAPQ;
                                                                                                                                                                                                                                                                                                                                                                                                          PF00084; sushi;
                                                                                                                                                                                                                                                                                             ; PS01180; CUB; 2.
; PS00022; EGF_1; FALSE_N
; PS01186; EGF_2; 1.
; PS01187; EGF_CA; 1.
; PS01187; EGF_CA; 1.
; PS00134; TRYPSIN_HIS; F
; PS00134; TRYPSIN_SER; 1
Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            ); IPR000859; CUB_domain.
); IPR001314; Chymotrypsin.
); IPR000561; EGF-like.
); IPR001881; EGF-Ca.
                                                                                                                                                                                                                                                                          doma:
                                                                                                                                                                                                                                                                                                                                                                                                                IPR001254; Ser_protease_Try.
IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000152; Asx_hydroxyl.
                             705
                                    146
161
176
193
250
309
338
338
376
406
451
451
650
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184
184
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183
193
308
375
502
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5221
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531
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA51851.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAA28407.1;
                             AA;
                                                                                                                                                                                                                                                                                 Phosphorylation;
                                                                                                                                                                                                                                                                          3D-structure.
                                                                                                                                                                                                                        463
705
141
190
305
372
                                                                                                                                                                                                                                                                                Plasma; Glycoprotein; Serine protease; Hydrolase; phorylation; Sushi; Repeat; Signal;
                             80173
       34.0%;
44.1%;
                                                                                                                                                                                                                                                                                                                                  FALSE_NEG
                             ME.
<u>ن</u>
                                                                       PROBABLE.
PROBABLE.
PROBABLE.
PROBABLE.
PROBABLE.
                                                                                                                                                                                           SERINE
CHARGE
CHARGE
                                                                                                                                                                                                                CUB 2.
SUSHI 1.
SUSHI 2.
             Score
                                    S
Pred. No. 0.0.
5; Mismatches
                                                         PROBABLE.
                                                                                                                                                                            CHARGE RELAY SYSTEM. HYDROXYLATION.
                          POTENTIAL.
S -> L (IN REF. 2).
5CBCCC0201061463 CRC64;
                                                 POTENTIAL.
                                                                                                                                  PROBABLE
                                                                                                                                          N-LINKED
                                                                                                                                                N-LINKED
                                                                                                                                                        N-LINKED
                                                                                                                                                               N-LINKED
                                                                                                                                                                     PHOSPHORYLATION (BY CK2).
                                                                                                                                                                                                                                      EGF-LIKE,
                                                                                                                                                                                                                                              CUB 1
                                                                                                                                                                                                                                                    COMPLEMENT
                                                                                                                                                                                                                                                                                                       FALSE_NEG
              81;
                                                                                                                                                                                          RELAY SYSTEM
                                                                                                                                                                                                          PROTEASE
                                                                                                                                        GLCNAC . .).
GLCNAC . .).
GLCNAC . .).
                                                                                                                                                                                                                                     CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                    C1R
C1R
              DB 1;
                                                          (PROBABLE).
       .04;
                                                                                                                                                                                                                                                    HEAVY
              Length 705;
                                                                                                                                                                                                                                                    CHAIN
Indels
0;
Gaps
0;
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PRESCULTION PRODUCTION PRODUCTION
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Q15113; O145
30-MAY-2000
                                                                                                                          "Post-translational proteolytic processing of procollagen C-
proteinase enhancer releases a metalloproteinase inhibitor."
J. Biol. Chem. 275:1384-1390(2000).
-:- FUNCTION: BINDS TO THE COOH-TERMINAL PROPEPTIDE OF TYPE
                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta; PubMed=9933570; MEDI,INE=99134301; PubMed=9933570; Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.; Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.; Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.; Scott I.C., Greenspan D.S.; Book I.C., Hoffman G.G., Hoffman G.G., Greenspan D.S.; Book I.C., Hoffman G.G., Hoffman G.G., Greenspan B.S.; Book I.C., Hoffman G.G., Hoffm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gloeckner G., School A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I procollagen C-proteinase enhancer) (Type 1 procollagen C-proteinase enhancer)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                              +
                                                                                                                                                                                                                                                                                        Mott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analysis of 650 kb of reveals 17 genes.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identification, primary structure, and
cognate human gene (PCOLCE).";
J. Biol. Chem. 269:26280-26285(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takahara K., Kessler E., Biniaminov L., B
Jani-Sait S., Shows T.B., Greenspan D.S.,
"Type I procollagen COOH-terminal protein
identification, primary structure, and ch
                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE, MEDLINE-20092917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hirahara
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                             Banda M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99018118; PubMed=9799793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morisaki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteinase enhancer protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Large-scale sequencing of two regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Smooth muscle cell derived procollagen C-protease enhancer protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jnpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kessler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95014462; PubMed=7523404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
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                                                              PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-FUNCTION: C-TERMINAL PROCESSED PART OF
      SUBCELLULAR LOCATION:
                                    METALLOPROTEINASE INHIBITORY ACTIVITY.
                                                                                                                                                                                                                                                                                        J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Struct. Funct. 21:662-662(1996).
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                                                                                                                                                                                                                                                                                        Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8:1060-1073(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Syoufuda K.,
Saito Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                 AND CHARACTERIZATION OF INHIBITORY ACTIVITY PubMed=10625689; C.L., Rosenbach M.T., Takahara K., Greenspa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
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      Secreted
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                                                                                               C-PROTEINASE
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localization
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                                                                                                                                                                                                                                                                                        Greenspan
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                                                                 MAY HAVE
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Query Match
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Matches 17
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SEQUENCE
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SITE
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                               SEQUENCE FROM N.A.
MEDLINE=89017187; PubMed=2459702;
Kusumoto H., Hirosawa S., Salier J.P.,
"Human genes for complement components
                                                                                                       Homo sapiens (Human).
Homo sapiens (Human).
'arvota; Metazoa; Chordata; (
'haria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                  SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                          SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A. TISSUE Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
SIGNAL
                                        tail-to-tail arrangement."
                                                                                                      NCBI_TaxID-9606;
                                                                                                                                                           Complement Cls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nterPro; IPR000859; CUB_domain.nterPro; IPR001134; Netrin_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute.
                                                                                                                                                                                                                                                                            PNYTRPVELCGGDVKGESGYVASEGFPNLYPPNKECIWTITVPEG
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                               Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:8738; PCOLCE.
                                                                                                                                                                                                                                                                                                                     . Similarity 37.8
17; Conservative
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tein; Repeat; Signal.
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                            85:7307-7311(1988)
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-LINKED (GLCNAC. . .) (POTENTIAL)
3D88430158648796 CRC64;
                                                                                                                                                                                                              Q9UCU9; Q9UCV0;
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                                                                                                                                                         (EC 3.4.21.42)
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                                                  Hagen F.
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C1s
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                                                  Kurachi K.;
in a close
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"Structure of the cataling study by chemics"
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Hess D., Schaller J., Rickli E.E.
"Identification of the disulfide
Biochemistry 30:2827-2833(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-86164350; PubMed-3007145;
Spycher S.E., Nick H., Rickli E.E.;
"Human complement component Cls. Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tosi M., Duponchel C., Meo T., Couture-To "Complement genes CIr and Cls feature an domain closely related to haptoglobin."; J. Mol. Biol. 208:709-714(1989).
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Tosi M., Duponchel C., Meo T., Julier C.;
"Complete cDNA sequence of human complement Cl
linkage of the homologous genes Cls and Clr.";
Biochemistry 26:8516-8524(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the heavy chain and identification activation.";
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Dragon-Durey M.-A.,
de Barace C., Prieu
                                       PubMed=11390518;
                                                                                                                                                                                                               PARTIAL SEQUENCE, MEDLINE-95298736;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 438-500;
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"Two lineac
                                                           DISEASE
                                                                                               Biochemistry
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lineages of mannose-binding
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                                                                                             34:7311-7321(1995).
   Prieur
                                                                                                                                 catalytic region cross-linking and
                                                                                                                                                                                                             AND 3D-STRUCTURE PubMed=7779774;
                 Quartier P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503-534;
   A.-M.,
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Fremeaux-Bacchi
s L., Fridman W.
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                                                                                                                                   three-dimensional
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Pfam; PF00008; EGF; 1.
Pfam; PF000084; sushi; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF000431; CUB; 2.
Pfam; PF000431; CUB; 2.
NART; SM00032; CCP; 2.
NART; SM00042; CUB; 2.
SMART; SM00042; TYP_SPC; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00179; TYP_SPC; 1.
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PIR; /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular basis of a selective C1s deficiency associated with early onset multiple autoimmune diseases.";
                                                                                                                                      Complement pathway; Hydroxylation; Sush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A40496; C1HUS.
PIR; S00224; S00224.
MEROPS; S01.193; -.
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000859; CUB_domain.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001561; EGF-1ike.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                           SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPONENT C2 TO C2A AND C2B.

COMPONENT C2 TO C2A AND C2B.

SUBUNIT: C1 IS A CALCIUM DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R AND S IN THE MOLAR RATION OF 1:2:2. ACTIVATED C1S IS AN DISULFIDE LINKED HETERODIMER OF AN HEAVY CHAIN AND A LIGHT CHAIN.

DISEASE: Defects in C1S are the cause of selective C1s deficiency, that is associated with early onset multiple autoimmune diseases. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.

SIMILARITY: CONTAINS 2 CUB DOMAINS.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: CLEAVES COMPONENT C4 TO C4A AND C4B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120580;
                                                                                                                                                             "E; PS00010; ASX_HYDROXYL; 1.

FE; PS01180; CUB; 2.

FE; PS00012; EGF_1; FALSE_NEG.

FE; PS01186; EGF_2; FALSE_NEG.

FE; PS01187; EGF_CA; 1.

FE; PS0240; TRYPSIN_DOM; 1.

FE; PS00134; TRYPSIN_SER; 1.
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                                                                                                                                      Sushi;
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172
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422
                                                                                                                                   Plasma; Glycoprotein; Serine protease; Hydrolase;
i; Repeat; Signal; EGF-like domain;
            SUSHI
                                         CUB
                                                                                COMPLEMENT
SERINE PROTEASE
                                                    EGF-LIKE,
              2 ب
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                                                    CALCIUM-BINDING (POTENTIAL)
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PACE TO THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDILINE-95014462; PubMed-7523404;
Takahara K., Kessler E., Biniaminov L., Brusel M., Eddy R.L.,
Jani-Sait S., Shows T.B., Greenspan D.S.;
"Type I procollagen COOH-terminal proteinase enhancer protein:
identification, primary structure, and chromosomal localization
cognate human gene (PCOLCE).";
J. Biol. Chem. 269:26280-26285(1994).
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961398; 035113;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Procollagen C-proteinase enhancer protein precursor (PCPE) (Type
procollagen COMH-terminal proteinase enhancer) (Type 1 procollagen
                                                                                                                                                                      Hirahara I., Syoufuda K., Harada K., Tomita M., Urakami K., Morisaki N., Saito Y.; "Smooth muscle cell derived procollagen C-protease enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
the choroid plexus and leptomeninges.";
J. Neurochem. 56:2133-2138(1991).
                                Lecain E., Zelenika D., Laine M.C., Rhyno "Isolation of a novel cDNA corresponding
                                                                         STRAIN=C57BL/6; TISSUE=CNS; MEDLINE=91225708; PubMed=2027019;
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                                                                                                                                                         Struct. Funct.
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                                                                                                              N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           derived procollagen C-protease 21:662-662(1996).
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G -> GG (IN REF. 5).
T -> A (IN REF. 7).
TK -> GR (IN REF. 7).
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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N-LINKED (GLCNAC . . ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN
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                                                     Rhyner T.,
                                                                                                                                                                                                                                                                                                                                        chromosomal localization
                                    to
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                                    transcript expressed
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                                                                                                                                                                          enhancer protein.";
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Best Local
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CONFLICT
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DOMAIN
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EMBL; X57337; CAA40612.1; ALT_FRAME.
MGD; MGI:105099; Pcolce.
InterPro; IPR000859; CUB_domain.
InterPro; IPR001134; Netrin_C.
                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                           Pfam; PF00431; CUB; 2
Pfam; PF01759; NTR; 1.
SMART; SM00042; CUB; 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Type I procollagen C-proteinase from mouse fibroblasts. Purification and demonstration of a 55-kDa enhancer glycoprotein."; Eur. J. Biochem. 186:115-121(1989).
                                                                                                                                   SEQUENCE
                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                    lycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kessler E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91076903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90092088; PubMed=2689170, Kessler E., Adar R.;
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CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          npublished observations (JAN-2000).

1- FUNCTION: BINDS TO THE COOH-TERMINAL PROCOLLAGEN AND ENHANCES PROCOLLAGEN
                                                                                                                                                                                                                             ROSITE; PS01180; CUB; 2.
lycoprotein; Repeat; Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: EXPRESSED IN INTERSTITIAL CONNECTIVE TISSUES
LIKE TENDONS, CALVARIA, SKIN AND AT A LOWER LEVEL IN HEART AND
                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 2 CUB DOMAINS. SIMILARITY: CONTAINS 1 NTR DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKELETAL MUSCLE
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                                                       PNYTRPVFLCGGDVTGESGYVASEGFPNLYPPNKKCIWTITVPEG
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                                                                         ----GRLASPGFPGEYANDQERRWTLTAPPG
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468
                                                                                                     31.1%;
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                                                                                                     Score 74;
Pred. No.
                                                                                                                                         N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .) (POTENTIAL).
D -> Y (IN REF. 3).
                                                                                                                                                                     CUB 2.
                                                                                                                                                                                                PROTEIN.
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           PRT;
                                                                                                                                 F9B55558147FABAB CRC64;
                                                                                            Mismatches
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                                                                                                     0.17;
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           B
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                                                                                                              Length 468;
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Pfam; PF00
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DOMAIN
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                                            PROSITE;
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36
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Kessler E., Mould A.P., Hulmes D.J.S.;

"Procollagen type I C-proteinase enhancer is a naturally connective tissue glycoprotein.";

Biochem. Biophys. Res. Commun. 173:81-86(1990).

-i- FUNCTION: BINDS TO THE COOH-TERMINAL PROPERTIDE OF TYPE PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-PROTEINASE ACTION: Secreted.

-i- SUBCELLULAR LOCATION: Secreted.

-i- SUBCELLULAR LOCATION: Secreted.

-i- TISSUES, ESPECIALLY TENDON. ALSO EXPRESSED IN CONTAINS 1 NTR DOMAINS.
                                                                                                                                                                                                   EMBL; U94710; AAB93478.1; -. EMBL; AB008534; BAA23317.1; -. EMBL; AF016503; AAD01592.1; -. EMBL; AF016506; AAD01598.1; -. InterPro; IPR000859; CUB_domain. InterPro; IPR001134; Netrin_C.
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Procollagen C-proteinase enhancer protein precursor (
procollagen COOH-terminal proteinase enhancer) (Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a continuous the EMBL between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Masuda M., Igarashi H., Kano M., Yoshikura H.; "Proviral integration into the procollagen C-proteinase e protein gene and its effects in cultured rat fibroblasts an excisable 'hit-and-run' retroviral vector."; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
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Morisaki N., Saito Y.;
"Smooth muscle cell derived procollagen C-pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97447750; PubMed=9303490;
Ogata I., Auster A.S., Matsui A., Greenwel P., Geerts A., [
Fujiwara K., Kessler E., Rojkind M.;
"Up-regulation of type I procollagen C-proteinase enhancer
messenger RNA in rats with CC14-induced liver fibrosis.";
Hepatology 26:611-617(1997).
                                                                                                                                       Pfam; PF01759; NTR; SMART; SM00042; CUB
                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                              Repeat; Si
                                                                                                                                                                                     CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Aorta;
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468
                                                                                                                                                                                                                                                                                                                                                                                         license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
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                                           PROCOLLAGEN C-PROTEINASE ENHANCER
                                                                   POTENTIAL
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e 1 proc
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; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IN COLLAGEN-RICH ORNEA AND STERNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E TYPE I ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restrictions
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procollagen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collaboration
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RESULT 10
UVS2_XENLA
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Best Local Similarity
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    his SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
11-NOV-1997 (Rel. 35, Last sequence update)
11-NOV-1997 (Rel. 35, Last sequence update)
5-JUN-2002 (Rel. 41, Last annotation update)
5-JUN-2002 (Rel. 41, Last annotation update)
Embryonic protein UVS.2 precursor (EC 3.4.24.-).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P42664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UVS2
                                                                                                              InterPro; IPR001506; Astacin.
InterPro; IPR000859; CUB_domain
InterPro; IPR000130; Zn_MTpeptds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=97228908; PubMed=9074934;
                                          SMART; SM00042; CUB; 2.
SMART; SM00235; ZnMC; 1.
                                                                                                                                                                                                    EMBL; D89632;
                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sato S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression in hatching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Katagiri C., Maeda
Yasumasu S.;
                 PROSITE;
                                                                        PRINTS; PRO0480;
                                                                                                                                                            MEROPS; M12.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90108413; PubMed=1688538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 196-514 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 PNYTRPVFLCGGDVTGESGYVASEGFPNLYPPNKKCIWTITVPEG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A. SIMILARITY: CONTAINS 2 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                      Lecular approach to dorsoanterior development in x Biol. 137:135-141(1990).

GOFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

DEVELOPMENTAL STAGE: EXCLUSIVELY IN THE ANTERIOR NEURULA STAGE EMBRYOS. BY THE TALLBUD STAGE, THE ELOCALIZED IN SPECIALIZED CEPHALIC ECTODERM, IN A CORRESPONDING TO THE HATCHING GLAND.
                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bloinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Dev. Biol.
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                                                                                    PF00431; CUB; 2.
PF01400; Astacin; 1.
                                                                                                                                                                         P07584;
              PS00142; ZINC_PROTEASE; PS01180; CUB; 2.
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352
28
454
468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cloning of Xenopus hatching enzyme and
in hatching gland cells.";
v. Biol. 41:19-25(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sargent T.D.;
Metalloprotease; Zinc; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                         1IAE
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461
28
454
50185 1
                                                                      ASTACIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R., Yamashika
                                                                                                                Zn_MTpeptdse
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N-LINKED (GLCNAC. . .) (POTENTIAL)
; B4AA1C151323969B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 74; DB 1
Pred. No. 0.17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K., Sargent T.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis.";
                                                                                                                                                                                                                                                                                                                                                                                      REGION PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                 NEURAL
                                                                                                                                                                                                                                                                                                     EMBL
                                                                                                                                                                                                                                                                                                    a collaboration - MBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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057460;
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CARBOHYD
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METAL
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Mini fin protein).
TOLLOID OR TLD OR MFN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dorsal-ventral patterning tolloid protein precursor (EC 3.4.24..)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
CHAIN
                                                   between
                                                               This SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                                                         Development 126:3119-3130(1999).
                                                                                                                                                                                                                                                                                             Connors S.A., Trout J., Ekker M., Mullins M.C.; "The role of tolloid/mini fin in dorsoventral pattern
                                                                                                                                                                                                                                                                                                                         FUNCTION, AND TISSUE SPECIFICITY. MEDLINE=99307076; PubMed=10375503;
                                                                                                                                                                                                                                                                                                                                                               Blader P., Rastegar S., Fischer N., "Cleavage of the BMP-4 antagonist c. Science 278:1937-1940(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinopterygii; Neopterygii; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                  zebrafish embryo."
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98057457; PubMed=9395394;
                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Gastrul
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17
                                                                                        tailbud and cranial neural crest. At the 20-somite stage, also expressed in the hematopoletic system.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                  FUNCTION: Required for patterning ventral tissues of the tail. May increase bone morphogenetic protein (BMP) activity at the end of gastrulation by proteolytic cleavage of chordin and release of BMP from inactive complexes.

TISSUE SPECIFICITY: During gastrulation, accumulates around the
                                                                                                                                                        closing blastopore with greater expression ventrally. animal pole, expressed in the ectoderm flanking the anneural plate. At the 10-somite stage, expressed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPGFPGEYANDQERRWTLTAPPGYR 41
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                                                  the Swiss Institute of Bioinformatics
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514
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ZINC (CATALYTIC) (BY SIMILARITY).

N'LINKED (GLCACC...) (POTENTIAL).

N'LINKED (GLCNAC...) (POTENTIAL).
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Teleostei; Ostariophysi; Cypriniformes;
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hordin by zebrafish Tolloid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1022 AA
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0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                               formation of the
                                                                                                                                                            the developing
                                                                                                                                                                          anterior
                                                   EMBL outstation
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                                                                                                                                                                                      the
                                                                collaboration
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SIGNAL
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PROSITE; PS001180; CUB; 5.

PROSITE; PS01180; CUB; 5.

PROSITE; PS01186; EGF_2; PS01186; EGF_2; 2.

PROSITE; PS01187; EGF_CA; 2.

PROSITE; PS01142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00008; EGF; 2.
Pfam; PF00431; CUB; 5.
Pfam; PF01400; Astacin; 1.
PRINTS; PR00480; ASTACIN.
                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00042; CUB; 5.
SMART; SM00181; EGF; 2.
SMART; SM00179; EGF_CA; 2.
MART; SM00235; ZnMC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZFIN; ZDB-GENE-990415-265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [nterPro;
 Local Similarity hes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF027596; AAC60304.1; P35555; 1EMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M12.016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001506; Astacin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             email to license@isb-sib.ch).
                                                                157
358
471
583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
33
157
   Conservative
                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                   1012
1012
249
250
253
253
384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357
              31.1%;
                                                                115536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF-like domain;
                                                        BY SIMILARITY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tolloid
                                                                                                                                                                                                                                                                                                                                ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
 8
Pred. No. 0.38
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUB
                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF-LIKE 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
DORSAL-VENTRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF-LIKE 2, CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protease; Metalloprotease; Zinc;
lomain; Repeat; Signal; Glycoprotein;
              DB 1;
0.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATTERNING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY
                             Length 1022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                               CRC64;
 Indels
                                                                         ) (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
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0
Gaps
0
 RESULT 12
CASP_MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
         Pfam; PF00008; EGF; 1.
Pfam; PF00084; SUSh1; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF000431; CUB; 2.
Pfam; PF00722; CHYMOTRYPSIN.
SMART; SM00032; CCCP; 2.
SMART; SM00042; CUB; 2.
SMART; SM00010; EGF_CA; 1.
SMART; SM00100; Tryp_SPc; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CASP_MESAU STAI
P15156;
01-APR-1990 (Rel. :
01-APR-1990 (Rel. :
15-JUN-2002 (Rel. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       capable of degrading extracellular matrix protein FEBS Lett. 250:411-415(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calcium-dependent serine proteinase precursor (EC 3.4.21.-) (CASP).
                                                                                                                                                                    InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001561; EGF-like.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR001881; EGF_CCF.
InterPro; IPR001436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                  MEROPS; S01.193;
                                                                                                                                                                                                                                                                                                                 PIR; S05008; S05008.
                                                                                                                                                                                                                                                                                                                                  EMBL; X16160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kinoshita H., Sakiyama H., Tokunaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mesocricetus.
NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: CAPABLE OF DEGRADING EXTRACELLULAR MATRIX PROTEINS CASP DEGRADES TYPE I AND IV COLLAGEN AND FIBRONECTIN IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isono K., Sakiyama S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89325606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            792 GTISSPNWPDKYPSRKECTWDITATPGHR 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRESENCE OF CALCIUM.

SUBUNIT: HETERODIMER, CONSISTING OF HEAVY AND LIGHT CHAINS WITH DISCULFIDE BONDS. THE HEAVY CHAIN IS EXPECTED TO BE A REGULATORY SUBUNIT AND THE LIGHT CHAIN CONTAINS THE CATALYTIC SITE.

DOMAIN: THE GLU-RICH REGION IN THE N-TERMINAL REGION MAY BE GAMMA CARBOXYLATED AND FUNCTION AS A CALCIUM-BINDING SITE.

SIMILARITY: TO BLOOD COAGGLATION FACTORS SUCH AS IX, X AND AN ANTICOAGGLATION FACTOR, PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO REPTIDASE FAMILY S1.
SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRLASPGFPGEYANDQERRWTLTAPPGYR
                                                                                                                                                                                                                                                                                                    1.DPO
                                                                                                                                                                                                                                                                                                                                  CAA34286.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=2753140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               695
                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Imajoh-Ohmi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins.
                                                                                                                                                                                                                                                                                                                                                                                              Usage
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BMP1_
                                                                                                                                                                                                                                                                                               RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                      BMP1_HUMAN STANDARD; PRT; 986 AA.
P13497; 013292; 099421; 099422; 099423; 014874; 090L38; Q13872;
01-JAN-1990 (Rel. 13, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
5-JUN-2002 (Rel. 41, Last annotation update)
5-JUN-2002 (Rel. 41, Last annotation update)
One morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mTld).
                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                      _HUMAN
                    Kriz
                                                                             is identical protein-1.";
                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM BMP1-3).
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Serine protease; Calcium-binding; Extracellular matrix; Gamma-carboxyglutamic acid; Vitamin K; Hydroxylation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                          Prockop D.J.
                                                                                                                                        TISSUE=Skin;
                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                             Wozney J.M.,
                                                                                                                   Li S.W.,
                                                                                                                              MEDLINE=96209868;
                                                                                                                                                                                              Homo sapiens (Human)
                                      MEDLINE=89072730; PubMed=3201241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
        Nozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitte Criz R.W., Hewick R.M., Wang E.A.;
Novel regulators of bone formation: molecular clones and
                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMAIN
                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                               9
                                                                                               C-proteinase
                                                                                                                                                                                                                                                                                                                                              EP-VFGRLASPGFPGEYANDQERRWTLTAPPGY 40
                                                                                                                                                                                                                                                                                                                           EPTMHGEILSPNYPQAYPNEMEKTWDIEVPEGF
                                                                                                                                                                                                                                                                                                                                                                 l Similarity
12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-like domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00022;
PS01186;
PS01187;
PS50240;
PS00134;
                                                                                                                   Sieron A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00135;
                                                                                                                                                                                                                                                                                                                                                                                                        695
                                                                                                                                                                                                                                                                                                                                                                                                                       164
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181
297
297
352
445
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155
1638
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                                                                                       to the
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22
                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                that
                                                                  Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF_CA; 1.
TRYPSIN_DOM; 1.
TRYPSIN_HIS; FALSE_NEG.
TRYPSIN_SER; 1.
                                                                                                                           PubMed=8643539;
                                                                                                                                                                                                                                                                                                                                                                                                                                  124
136
296
349
415
695
178
155
178
155
1536
638
1536
153
153
153
153
153
                                              (ISOFORM BMP1-1).
                                                                                                                                                                                                                                                                                                                                                                                                      413
77493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444
                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                         081
                                                                                                                                                                                                                                                                                                                                                                         30.5%;
                                                                                                                    Fertala
                                                                                    processes procollagens to fibrillar collagens otein previously identified as bone morphogenio
                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                        X
                                                                                                                                                                                                                                                                                                                                                                Score 72.5; [
Pred. No. 0.39
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUSHI 1.
SUSHI 2.
                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

OF CONTROL (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

E924F7E6340700D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUB 2.
SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-LIKE, CALCIUM-BINDING (POTENTIAL). HYDROXYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CALCIUM-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALCIUM-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALCIUM-DEPENDENT
                                                                                                                   A., Hojima Y.,
                                                                                                                                                                           Craniata; Vertebrata; Catarrhini; Hominidae
                                                                    93:5127
                           Mitsock L.M., Whitters
                                                                                                                                                                                                                                                                                                                                                                         DB
.39;
                                                                                                                                                                             Hominidae;
                                                                                                                   Arnold W.V.,
                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SERINE
SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY
(BY)
                                                                                                                                                                                                                                                                                                                                                                                  Length 695;
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              / SIMILARITY).
/ SIMILARITY).
/ SIMILARITY).
                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEINASELIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEINASE HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEINASE
                                                                                      morphogenic
                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                 1;
MIM;
                                                                                                                                                                                              Genew;
                                                                                                                                                                                                                                                                                                               or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-P
                                                                                                                            InterPro;
                                                                                                                                      InterPro;
                                                                                                                                               InterPro;
                                                                                                                                                         InterPro;
                                                                                                                                                                   InterPro;
                                                                                                                                                                           InterPro;
                                                                                                                                                                                                        MEROPS;
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SOTTTTTTTT

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EMBL; U50330; AAA93462.1; -.
EMBL; W22488; AAA51833.1; -.
EMBL; Y08723; CAA69973.1; -.
EMBL; Y08724; CAA69974.1; -.
EMBL; Y08725; CAA69975.1; -.
EMBL; L35278; AAC41703.1; -.
EMBL; L35279; AAC41701.1; -.
                                      PROSITE; PS00142; PROSITE; PS01180; PROSITE; PS00010; PROSITE; PS00022; PROSITE; PS01186; PROSITE; PS01186; PROSITE; PS01186; PS0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                             PRINTS; PR00480; ASTACIN.
SMART; SM00042; CUB; 5.
SMART; SM00179; EGF_CA; 2.
SMART; SM00235; ZnMC; 1.
                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF000008; EGF; 2. Pfam; PF00431; CUB; 5. Pfam; PF01400; Astacin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takahara K., Lyons G.E., Greenspan D.S.;
"Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld)
are encoded by alternatively spliced transcripts which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 differentially expressed in some tissues."; J. Biol. Chem. 269:32572-32578(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Janitz M., Heiser V., Boettcher U., Le "Three alternatively spliced variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 242:1528-1534(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P00736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A37278; A37278.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98160316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alternative splicing.
TISSUE SPECIFICITY: UBIQUITOUS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND II. INDUCES CARTILAGE AND BONE FORMATION. CATALYTIC ACTIVITY: Cleavage of the C-terminal Ala-1-Asp in type I and II procollagens and at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENDOPEPTIDASE ENHANCER PROTEIN.
ALTERNATIVE PRODUCTS: 7 isoforms;
here), BMP1-4, BMP1-5, BMP1-6 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFACTOR: BINDS 1 ZINC ION (BY ENZYME REGULATION: ACTIVITY IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Siol. Chem. 269:32572-32578(1994).
FUNCTION: CLEAVES THE C-TERMINAL PROPERTIDES OF PROCOLLAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           morphogenetic protein-1.";
ol. Med. 76:141-146(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001506; Astacin.
IPR000152; Asx_hydroxyl.
IPR000859; CUB_domain.
IPR000561; EGF-like.
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IPR000130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             equires a license agreement (See http://www.isb-sib.ch/announce/
email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1APQ.
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CUB; 5.

ASX_HYDROXYL; 2.

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EGF_2; 2.

EGF_CA; 2.
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                                                                                                                                                                                          ZINC_PROTEASE;
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INCREASED BY
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BMP1-7;
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e; EGF-like domain; Zinc; Calcium; Signal;
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POTENTIAL.
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ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

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CUB 2.
EGF-LIKE 1,
CUB 3.
                                                                                                                                      PQEGSYLDFWDTHRGDPKPRRRKSLKTFSLTPÄTFRGIWA
L (IN ISOFORM BMP1-7).
MISSING (IN ISOFORM BMP1-7).
D -> N (IN REF. 4).
R -> S (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGRPHOLKFRYOKRNERPEQ (IN ISOFORM BMP1-1).
MISSING (IN ISOFORM BMP1-1).
OEYNFI.KMEDDEVERT
                                                                                                                                                                                                                                                                                                 ISOFORM BMP1-5).

MISSING (IN ISOFORM BMP1-5).

DKDECSKONGGCQQD -> GGELFGLLGHPPRRP
ISOFORM BMP1-6).

MISSING (IN ISOFORM BMP1-6).
                                                                                                                                                                                                                      -> VLEGAGDRHSHLSGLELLLCPHALVDTVPAPPSALHGD
THAHTHTHVHTHCPIAQETCRGPPLGASRLSPQGPGHLTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                             QEYNFLKMEPQEVESLGETYDFDSIMHYARNTFSRGIFLDT
IVPKYEVNGVKPPIGQR -> VLHSSLLLLSCGSRNGASFP
CSLESSTHQALCWTGLFLRPSPFPRLPLAAPRTLRAGV
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CUB 4.
                                                                                                                                                                                                                                                    VKLTFMEMDIESQPECAYDHLEVFDGRDAKAPVLGRFCG
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                                                                                                                                                                                                                                                                                DKDECSKDNGGCQQDCVNTFGSYECQCRSGFVLHDNKHDCK
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DLQVGKPLLWDRHCFRLSTHGPEMLGTALRG (IN
                                                                                                                                                                                                                                                                                                                                                                                                                 (IN ISOFORM BMP1-4).
MISSING (IN ISOFORM BMP1-4)
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                                                                                                                      -> N (IN REF. 4).
-> S (IN REF. 4).
F89201913AC3CBEA CRC64;
                                                             Mismatches
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                             41
                                                                                         DB 1;
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                                                             12;
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RESULT 14 BMP1\_MOUSE

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PRINTS; PRO0480; ASTACIN.
SMART; SM00142; CUB; 5.
SMART; SM00179; EGF_CA; 2.
SMART; SM00235; ZNMC; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS001180; CUB; 5.
PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS001186; EGF_2; 2.
PROSITE; PS01186; EGF_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P98063;
01-FEB-1996
01-FEB-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                      InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;

"Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
which is related to the Drosophila dorsoventral gene tolloid and
encodes a putative astacin metalloendopeptidase.";

Dev. Biol. 163:175-183(1994).

-i- FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, I:
AND II. INDUCES CARTILAGE AND BONE FORWATION.

-i- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
Ala-1-Asp in type I and II procollagens and at Arg-1-Asp in type
               Glycoprotein;
SIGNAL
                                             PROSITE; PS01187; EGF_CA; 2.
Growth factor; Cytokine; Repeat; Bone; Metalloprotease; EGF-like domain; Zinc;
                                                                                                                                                                                                                                       Pfam; PF00008; EGF; 2.
Pfam; PF00431; CUB; 5.
Pfam; PF01400; Astacin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a copyre the swiss institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BMP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-FCB-2001 (Rel. 40, Last annotation update)
Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
(Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mTld).
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L24755; HSSP; P00736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6; TISSUE=Embryo; MEDLINE=94229342; PubMed=8174772;
                                                                                                                                                                                                                                                                                                                                                                                       MGD;
                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; M12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENDOPEPTIDASE ENHANCER PROTEIN.

TISSUE SPECIFICITY: AT HIGH LEVELS IN EMBRYONIC MATERNAL DECIDUUM
AND ELOOR PLATE REGION OF THE NEURAL TUBE. LESS IN DEVELOPING
AND ENDOCHONDRAL BONE, SUBMUCOSA OF INTESTINE, DERMIS
OF SKIN AND THE MESENCHYME OF SPLEEN AND LUNG.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: BINDS 1 ZINC ION (BY ENZYME REGULATION: ACTIVITY IS
                                                                                                                                                                                                                                                                                                                                                                 PS; M12.005; -.
MGI:88176; Bmpl.
rPro; IPR001506; Astacin
                                                                                                                                                                                                                                                                                 JPR000152; ASX_hydroxy1.
JPR000859; CUB_domain.
JPR000561; EGF-Like.
JPR0001881; EGF_Ca.
JPR000130; Zn_MTpeptdse.
; Zymogen.
1 25
26 125
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               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
INCREASED BY THE PROCOLLAGEN C-
                                                            Cartilage;
                                              Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                                             Hydrolase;
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IN DEVELOPING
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tent is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                    Ol-FEB-1996 (Rel. 33, Createu)
Ol-FEB-1996 (Rel. 33, Last sequence update)
I6-OCT-2001 (Rel. 40, Last annotation update)
Ione morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).
Ienopus laevis (African clawed frog),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                           MEDLINE-9085707; PubMed-8262384;
MEDLINE-904085707; PubMed-8262384;
Meno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;
Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;
Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;
Meno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;

"Cloning and expression of cDNA encoding Xenopus laevis bone
morphogenetic protein-1 during early embryonic development.";

Gene 134.257-261(1993).

-i- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER
DIFFERENTIATION OF DEVELOPING ORGANS.

-i- SUPPLOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED
TADPOLES; LITTLE OR NO EXPRESSION IN MOROLA AND LATE GASTRULA.

-i- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

-i- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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P98070;
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                   between
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                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
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             SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
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CUB 5.

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METALLOPROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
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Matches 13
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PÍAM; PEO0431; CUB; 3.

PÍAM; PEO1400; ASTACIN.

PRINTS; PRO0480; ASTACIN.

SMART; SM00042; CUB; 3.

SMART; SM00079; EGF_CA; 1.

SMART; SM000235; ZDMC; 1.

PROSITE; PS00142; ZINC_PROTE
PROSITE; PS001180; CUB; 3.

PROSITE; PS001180; CUB; 3.

PROSITE; PS00010; ASX, HYDRO)
PROSITE; PS001186; EGF_C3; 1.

PROSITE; PS001187; EGF_CA; 1.

PROSITE; PS01187; EGF_CA; 1.
                                                                                       BMPH_STRPU STAI

P98069;

01-FEB-1996 (Rel.

01-FEB-1996 (Rel.

16-OCT-2001 (Rel.
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ACT_SITE
METAL
             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bone morphogenetic protein 1 homolog precursor (EC 3.4.24.-)
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocent
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CARBOHYD
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Strongylocentrotus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                     GRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                               GSINSPGWPKEYPPNKNCIWQLVAPTQYR 591
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13; Conserv
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J. IPR001506; Astacin.

J. IPR000152; Asx_hydroxyl.

J. IPR000859; CUB_domain.

J. IPR000861; EGF-like.

J. IPR001881; EGF_CCA.
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10; ASX_HYDROXYL; 1.

10; ASX_HYDROXYL; 1.

10; EGF_1; FALSE_NEG.

186; EGF_2; 1.

187; EGF_CA; 1.

187; EGF_CA; 1.

187; EGF_CA; 1.
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                                                                                                                                                                    STANDARD;
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CUB; 3.
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EGF-
CUB
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                                                                                                                                                                                                                                                                                                                                         Mismatches
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D (GLCNAC. .
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                                                                                                                                                                                                                                                                                                                                                     DВ
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                 Strongylocentrotidae;
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SIMILARITY).
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(POTENTIAL).
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                                 Query Match
Best Local
                         Matches
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PRINTS; PR00480; ASTACIN.
SMART; SM00042; CUB; 2.
SMART; SM00179; EGF_CA; 1.
SMART; SM00235; ZnMG; 1.
                                                                               DISULFID
DISULFID
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CARBOHYD
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                                                                                                                                                                                                                                                                                                       PROSITE: PS00142; ZINC_PROTEASE: 1.
PROSITE: PS01180; CUB: 2.
PROSITE: PS00010; ASX_HYDROXYL; 1.
PROSITE: PS000022; EGF_1; FALSE_NEG.
PROSITE: PS01186; EGF_2; 1.
PROSITE: PS01187; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
InterPro;
InterPro;
                                                                                                                                                              METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hwang S.P.L., Partin J.S., Lennarz W.J.;
"Characterization of a homolog of human bone morphogenetic in the embryo of the sea urchin, Strongylocentrotus purpura Development 120:559-568(1994).

-I- TISSUE SPECIFICITY: ECTODERWAL AND PRIMARY MESENCHYM CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restitute to the European Bioinformatics institute.
                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L23838;
HSSP; P00736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                     ACT_SITE
                                                                                                                                                                                                METAL
                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                     Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; M12.005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94215496; PubMed=8162855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7668;
[1]
                                                                                                                                                                                                                                                                  detalloprotease; EGF-like domain;
IGNAL 1 23 POTE
PROPEP 24 109 POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [nterPro;
  13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE: EMBRYO; HIGHEST LEVEL SIMILARITY: BELONGS TO PETTIDASE FAMILY MISSIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN. SIMILARITY: CONTAINS 2 CUB DOMAINS.
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GRLASPGFPGEYANDQERRWTLTAPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00008; EGF; PF00431; CUB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            p; IPR001506; Astacin.
p; IPR000152; Asx_hydroxyl.
p; IPR000859; CUB_ddmain.
p; IPR000561; EGF_like.
p; IPR0001881; EGF_Ca.
p; IPR000130; Zn_MTpeptdse.
                                  Similarity
                                                                                                                                                                                               24
110
110
307
420
532
197
                         Conservative
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                                                                                                                                                                                                                                                                                                    protein;
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71893 MW;
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                                                                                                                                                                                                                                                                                                 Repeat; Hydrolase; Protease;
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                                                                                                                          BY SIMILARITY.
ZINC (CATALYTIC)
ZINC (CATALYTIC)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                 Score 66;
Pred. No.
                                                                                          N-LINKED
                                                                   N-LINKED (GLCNAC. . .) (P
59307B265B7894AD CRC64;
                                                                                                                                                                                            EGF-LIKE, CALCIUM ZINC (CATALYTIC)
                                                                                                                                                                                                                              BONE MORPHOGENETIC METALLOPROTEASE.
CUB 1.
                                                                                                                N-LINKED
                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                 SIMILARITY
                      Mismatches
                                                                                                                                                                                                                                                                                        Calcium;
                                                                               GLCNAC...)
GLCNAC...)
GLCNAC...)
GLCNAC...)
                                                                                                                                                                                             CALCIUM-BINDING (POTENTIAL).
ALYTIC) (BY SIMILARITY).
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There are no rest
ng as its content
                                            ВВ
                                             <u>ب</u>
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(BY
                                            Length 639;
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SIMILARITY)
                      Indels
                                                                                       ) (POTENTIAL).
) (POTENTIAL).
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                                                                               (POTENTIAL)
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RESULT 17
NRP1_CHICK
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                                                                                                          PRINTS; PRO0020; MAMDOMAIN.

SMART; SM00042; CUB; 2.

SMART; SM00231; FA58C; 2.

SMART; SM00137; MAM; 1.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01286; FA58C_1; 2.

PROSITE; PS01286; FA58C_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRP1_CHICK P79795;
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC TECTUM
(LAYERS D AND E OF SGFS), AMACRINE CELLS OF RETINA, NEURITES
DORSAL ROOT GANGLIA. ALSO EXPRESSED IN NONNEURONAL CELLS, E.G
BLOOD VESSELS IN THE ENTIRE EMBRYO.
-!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
-!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
-!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).

Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, I
16-OCT-2001 (Rel. 40, I
Neuropilin-1 precursor
                                                                                                                                                                                                                                                                                                              EMBL; D45416; BAA08256.1; -. HSSP; P12259; 1CZT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   developing chick nervous sys
Dev. Biol. 170:207-222(1995)
-!- FUNCTION: RECEPTOR INVOL
                                   SIGNAL
                                                Cell adhesion.
                                                                              PROSITE; PS00740; MAM_1; PROSITE; PS50060; MAM_2;
                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                     Ptam;
                                                                                                                                                                                                                                                                                 InterPro; IPR000859; CUB_domain
InterPro; IPR000421; FA58_C.
                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                           entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Expression of a cell adhesion molecule, neuropilin,
developing chick nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujisawa H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takagi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-White leghorn; TISSUE-Embryonic brain; mEDLINE-95324761; PubMed-7601310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRP1 OR NRP
                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                  InterPro; IPR000421;
InterPro; IPR000998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERV SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT OFFICE ACCOUNTS PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROPERTIES
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                                                                                                                                                                                                                     PF00629; MAM; 1.
PF00754; F5_F8_type_
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
1 precursor (A5 protein).
      1
19
20
                                                              Glycoprotein;
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    18
914
847
                                                                                                                                                                                                                                                                                                                                                                        license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                  MAM_domain
                                                              Neurone; Signal; Repeat; Receptor;
POTENTIAL.
NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL).
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COLLA9
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 Query Ma
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Colloalus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; C
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                                                                                                                                                                                                                                                                                                                                                                                 "Cartilage type IX collagen-proteoglycan camino-terminal globular domain encoded by J. Biol. Chem. 263:2324-2329(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishimura I., Muragaki Y., Olsen B.R.;
"Tissue-specific forms of type IX Collagen-proteoglycan arise the use of two widely separated promoters.";
J. Biol. Chem. 264:20033-20041(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Last sequence up 01-NOV-1995 (Rel. 32, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P12106;
01-OCT-1989
                                                                                                                                                                                                                                                    Proc.
                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 417-504 FROM N.A. MEDLINE=85216631; PubMed=3858862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-299 FROM N.A., AND PARTIAL SEQUENCE MEDLINE=88115376; PubMed=3339014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-416 FROM N.A. MEDLINE=90062114; PubMed=2584206;
                                                                                                                                                                                                                                                                                                       Lozano G., Ninomiya Y., Thompson H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                asios G., Nishimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 GRLASPGFPGEYANDQERRWTLTAPPGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                    collagen polypeptides.
oc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                                                    distinct class of vertebrate collagen genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
                                                                       DOMAIN: EACH SUBUNIT IS COMPOSED OF THREE TRIPLE-HELICAL DOMAINS DOMAINS. THE GLOBULAR DOMAIN AT THE NONCOLLAGENOUS DOMAINS. THE GLOBULAR DOMAIN AT THE N-TERMINUS OF TYPE IX COLLAGEN MOLECULES REPRESENTS THE NC4 DOMAIN WHICH MAY PARTICIPARE IN ELECTROSCRATIC INTERACTIONS WITH POLYANIONIC GLYCOSAMINOGLYCANS IN CARTILAGE.
                                                                                                                                                                                                          of the eye.
                                                                                                                                                                                                                                  FUNCTION: Structural
                                   PTM: Covalently linked to the telopeptides lysine-derived cross-links.
                                                                                                                                                                        3(IX) chain
                                                                                                                                                                                          SUBUNIT: Heterotrimer of a alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYLTSPGYPQSYHPSQKCEWLIQAPEPYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 B.R.;
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12; Conser
PROLINES AT THE THIRD POSIT: (G-X-Y) ARE HYDROXYLATED IN
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                   THE THIRD POSITION
                                                                                                                                                                                                                                                    S.A.
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                                                                                                                                                                                                                          82:4050-4054(1985).
Onent of hyaline cartilage and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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SIMILARITY.
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                                                                                                                                                                                        1(IX),
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2.9;
                   OF THE
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Phasianidae; Phasianinae;
ALL
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OF
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THE CHAINS
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RESULT 19
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   "Mutational analysis o
homolog.";
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P25723; O9VC46;
01-MAY-1992 (Rel. 2
01-MAY-1992 (Rel. 2
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                      01-MAY-1992 (Rel. 22, Created)
16-OCT-2001 (Rel. 40, Last annotation update)
Dorsal-ventral patterning tolloid protein pred
TLD OR CG6868.
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DISULFID
CONFLICT
CONFLICT
SEQUENCE
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           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-95324373; PubMed-7600963;
Finelli A.L., Bossie C.A., Xie T.,
Finelli A.L., analysis of the Drosop'
                                                                                    SEQUENCE FROM N.A.
STRAIN=Canton-S;
MEDLINE=92034970; PubMed=1840509;
Shimell M.J., Ferguson E.L., Childs S.R.,
"The Drosophila dorsal-ventral patterning human bone morphogenetic protein 1.";
                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brach
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsut the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentiations are supported to the statement of the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Cartilage; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M28659;
EMBL; J03539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
Development 120:861-870(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                      298
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                                                                                                                                                                                                                                                                                                                                                                                                                        Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS INTERRUPTED HELICES (FACIT) FAMILY.
                                                                             n bone morphogenetic 67:469-481(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A28360; A28360.
A28754; A28754.
B34493; B34493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; M28659; AAA48708.1;
; J03539; AAA48702.1;
; M11325; AAA48642.1;
; M11324; AAA48642.1;
                                                                                                                                                                                                                                                                                                                                                      PPGPPGPDGDAGKAGSPGLPGEPGAD-----GLTGPDG
                                                                                                                                                                                                                                                                                                                                                                          PLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ro; IPR000087; Collagen.
ro; IPR001791; Laminin_G.
ro; IPR003129; TSPN.
SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 16;
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417
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                                                                                                                                                                                                                                                                                                                                                                                                        27.5%;
                     the Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                Score 65.5; D
Pred. No. 1.8;
2; Mismatches
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                      gett R.W.
tolloid
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ION (N-TERMINAL) (NC4).
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                                                                                                   nnor M.B.
tolloid
                      gene,
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RA Hand R.C., Rogers, Y.-H.C. Blazej R.G., Champe M., Pfeliffer B.D., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Belson K.K., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Cadleu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dourbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Gudan P., Harris M., Harver D., Helman T.J., Hernandez J.R., Houck J., Harvey D., Helman T.J., Hernandez J.R., Houck J., Harvey D., Helman T.J., Hernandez J.R., Houck J., Alasin D., Houston K.A., Howland T.J., wei M.-H., Houck J., Lin X., Katlush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravttz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Li X., Liang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A., Mannel B.E., Spradling A.C., Stapleton M., Strong R., Sun E., Stapleton K., Siden K., Nixon K., Nusskern D.R., Pacleb J.M., Pallson D.L., Ra Alliams S.M., Woodage T., Weinsch M., Strong R., Sun E., Shen H., Woodage T., Weinscholer F., Shen H., Ra, Williams S.M., Woodage T., Weinschole, J., Wang X., Jang Q., Zhang L., Freitor C., Turner R., Venter E., Wang A.H., Wang X., Ra, Lin X., Mang S., Zhou X., Smith H.O., Park Sequence of Drosophila melanogaster.", The May Yumperature J.C., Scheelbach J., Schene J., Scheel J., Shong R., Shong L., Shong R., Shong J., Shong J.
                                         FlyBase; FBgn0003719; tld.
InterPro; IPR001506; Astacin.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000859; EGF-1ike.
InterPro; IPR0001881; EGF_Ca.
InterPro; IPR0001801; Zn_MTpeptdse.
InterPro; IPROO
InterPro; IPROO
InterPro; IPROO
InterPro; IPROO
Pfam; PFOOOO8; I
                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                       EMBL; M76976; AAA28491.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                       PIR; A39288; A39288.
HSSP; P00742; 1HCG.
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MEDLINE-20196006; PubMed-10731132;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                   MEROPS; M12.010;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS: MUTATIONS IN TLD GENE LEAD TO TRANSFORMATION OF DORSAL ECTODERM INTO VENTRA SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A. SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 5 CUB DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHYSICALLY WITH DPP-C PROTEIN
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C., Blazej R.G., Champe M., Pfeiffer B.D.,
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RESULT 20

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DT 16-0CT-2001

DT 16-0CT-2001

DT 16-0CT-2001
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PROSITE; PS001180; CUB; 5.
PROSITE; PS001010; ASX_HYDROXYL; 2.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 2.
Developmental protein; Hydrolase; Met
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SMART; SM00179; EGF_CA; 2.
SMART; SM00235; ZnMC; 1.
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PRINTS;
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                                                                                                                                        GSLYSPSYPDVYPNSKQCVWEVVAPPNH
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                                                                                                                                                                                                    Conservative
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1057
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                                                                                                                                                                                                                                                                120575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal;
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BY SIMILARITY.
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BY SIMILARITY
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                                                                                                                                                                                                                                 Length 1057
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( SIMILARITY)
( POTENTIAL)
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                                                                                                                                                                                                 0,
                                                                                                                                                                                                 Gaps
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(Rel. (Rel. (Rel.

40, Created)40, Last sequence update)40, Last annotation update)

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SMART; SM00042; CUB; 2:
SMART; SM00231; FA58C; 2:
SMART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2:
PROSITE; PS01285; FA58C_1; 2:
PROSITE; PS01286; FA58C_2; 2:
PROSITE; PS50060; MAM_2: 1.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Sprague-Dawley;
STRAIN-Sprague-Dawley;
MEDLINE=97433085; PubMed=9288754;
Kolodkin A.L., Levengood D.V., Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
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                        CARBOHYD
                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Neuropilin is a semaphorin III receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ginty D.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 90:753-762(1997).

1. 90:753-762(1997).

FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165 AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POPULATIONS OF THE CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE LINING IN THE RIBS.

SIMILARTY: BELONGS TO THE NEUROPILIN FAMILY.

SIMILARITY: CONTAINS 2 CUB DOMAINS.

SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00629; MAM; 1.
PF00754; F5_F8_type_C;
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                      149
208
277
434
152
157
629
833
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1 22
      AΑ;
                        CUB_domain.
FA58_C.
MAM_domain.
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    ₩;
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BY SIMILARITY.

N-LINKED (GLCNAC...

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CUB 2
F5/8
F5/8
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                                                                                                                                                                                                                                     MAM.
                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                          NEUROPILIN-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rowe E.G.,
                                                                                                                                                                                                                                                       TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
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    CRC64;
                                      (POTENTIAL).
(POTENTIAL).
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MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
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Search completed: January 11, 2003, Job time: 67 secs
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Best Local S
Matches 12
                                          27
                                                             2 PLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAP 37
                                       PCGGRLNSKDAGYITSPGYPQDYPSHQNCEWVYYAP
                                                                                 12;
                                                                                          Similarity
                                                                                 Conservative
                                                                                          26.9%;
                                                                                            Pred.
                                                                                                   Score
          10:49:28
                                                                                 Mismatches
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                                                                                                    64;
                                                                                                    DB 1;
                                        62
                                                                                 18;
                                                                                                  Length 925;
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0;

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Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number of hits satisfying chosen parameters:
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1: /SIDS2/gcgdata/g

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                                                                                                                                                                                                                                    5: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1984 DAT: *
6: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1985 DAT: *
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21: /SIDSZ/gcgdata/geneseg/genesegp-embl/AA2000 DAT: *
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## SUMMARIES

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238 93.5 93.5 93.5 93	238	Score
100.0 100.0 39.3 39.3 39.3 39.3 39.1	100.0	Query Match Length DB
. 686 1034 174 174 174 174 97	41 671	Length
23 23 22 22 22 21	23	DΒ
AAE14564 AAE14568 ABG21134 AAU87257 AAU197255 AAU19914 AAG01729 AAG007221	AAE14563 AAE14565	ID
MASP-2 MASP-2 human centra cDNA S human secret secret	Human 20 kDa MASP- Human mature MASP-	Description

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Human novel G-prot Gene 36 human secr Human polypeptide, Human smooth muscl Procollagen C-prot Human smooth muscl Human cancer assoc Human polypeptide,	Refine proteined	ase PRTS-1.

ALIGNMENTS

AAE14563 standard; peptide; 41 A

AAE14563;

17-MAY-2002 (first entry)

Human 20 kDa MASP-2 fragment

RESULT 1
AAEL4563
ID AAEL
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XX Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL; complement fixation; infection; microbe; retrovirus; HIV; abortion; human immunodeficiency virus; pathogenic bacteria; inflammatory disorder.

Homo sapiens.

WO200206460-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to use of a polypeptide derived from mannan-binding lectin (MBL) associated serine protease-2 (MASP-2) for producing a pharmaceutical composition. MASP-2 is a complement fixing enzyme and involved in lectin pathway of complement activation the pharmaceutical composition comprising MASP-2 is useful for the pharmaceutical composition comprising MASP-2 is useful for
                                                                                                                                                                                        Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL; complement fixation; infection; microbe; retrovirus; HIV; abortion; human immunodeficiency virus; pathogenic bacteria; inflammatory disorder
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                                                                                                                                                                                                                                                            Human mature MASP-2 protein.
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01-JUN-2001; 2001DK-0000870.
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AAE14565 standard;
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/note= "This region is specifically claimed claim 45"
                                                                                                              Location/Qualifiers 15..671
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                                             Region
                                                                                                                                    Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; mannan-binding lectin associated serine protease-2; MASP-2; MBL; complement fixation; infection; microbe; retrovirus; HIV; abortion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunodeficiency virus; pathogenic bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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16..686
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16..31
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16..56
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"This region is specifically claimed in claim
                                                                                                                                                                                                                                                                                                                                                     Signal_peptide
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Pred. No. 5.4e-22;
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                                                                                             The invention relates to use of a polypeptide derived from mannan-binding lectin (MBL) associated serine protease-2 (MASP-2) for producing a pharmaceutical composition. MASP-2 is a complement-fixing enzyme and involved in lectin pathway of complement activation. The pharmaceutical composition comprising MASP-2 is useful for treating infections caused by microbes such as fungus, yeast, the pharmaceuticum caused by microbes such as fungus, yeast,
                                                                                                                                                                                                                                 Use of a polypeptide comprising amino acid sequence derived from mannan-binding lectin associated serine protease-2 (MASP-2) for producing pharmaceutical composition, to treat bacterial, fungal,
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                                                                                                                                                                                                Claim 41; Fig
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MASP-2 inhibitor is useful for
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2001DK-0000870
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The region 30 to 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Encoded by C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note- "This region is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ′label• EGF-like_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label - CCP-2_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptides"
                                                                                                                                                                                                                                                                                                                                S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 307
                                                                                                                                                                                              English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Fragment obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clr/Cls-like_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is specifically claimed in claim 4 6 is specifically claimed in claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specifically claimed
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RESULT 4
AAE14568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                             Use of a polypeptide comprising amino acid sequence derived from mannan-binding lectin associated serine protease-2 (MASP-2) for producing pharmaceutical composition, to treat bacterial, fungal,
                                                                                                                                                                                                                                                                                                                                                                          Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders. The present sequence is human MASP-2 protein. Note: The present sequence is stated as being the same as SEQ ID NO:2 shown in sequence listing of the specification However the sequences differ at various locations.
                                                                                                                                                                               13-JUL-2000; 2000DK-0001089
01-JUN-2001; 2001DK-0000870
                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human MASP-2 protein, alternative version.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE14568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE14568 standard;
                                                                                                                                 Jensenius JC,
                                                                                                                                                   (JENS/) JENSENIUS J C. (THIE/) THIEL S.
                                                                                                                                                                                                           13-JUL-2001; 2001WO-DK00499
                                                                                                                                                                                                                                                  WO200206460-A2
                                                                                                                                                                                                                                                                                                                                                                                                                          human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                              2002-179791/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR
                                                                                                                                                                                                                                                                                                                                                                                                                         immunodeficiency virus; pathogenic bacteria; inflammatory disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                           mannan-binding lectin associated serine protease-2; MASP-2; MBL;
                                                                                                      AAD24224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   fixation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                 Thiel
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299
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1..15
                                                                                                                                                                                                                                                                                                                                                         /label= Signal_peptide
16..686
                                                                                                                                                                                                                                                                    /note-
                                                                                                                                                                                                                                                                                                          /note-
                                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                                                              /label= Mature_MASP-2_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100
                                                                                                                                                                                                                                                                                                                                                                                                                                    infection; microbe;
                                                                                                                                                                                                                                                                    "Encoded by
                                                                                                                                                                                                                                                                                     "Encoded by CAG'
                                                                                                                                                                                                                                                                                                          "Encoded
                                                                                                                                                                                                                                                                                                                            "Encoded by CA"
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                                                                                                                                                                                                                                                                    CCT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238; DB 23;
No. 5.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                   retrovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                viral
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The invention relates to use of a polypeptide derived from mannan-binding lectin (MBL) associated serine protease-2 (producing a pharmaceutical composition. MASP-2 is a complementation of the composition of the complementation of the composition of the composi

(MASP-2)

for

Page 71-73;

76pp;

English

as

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PF PD XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating infections caused by microbes such as fungus, yeast, retrovirus (e.g. human immunodeficiency virus (HIV)), or pathogenic bacteria which are resistant to at least one antibiotic medicament or multiresistant. The polynucleotide encoding MASP-2 is useful for treating patients deficient in MASP-2. The invention also discloses MASP-2 assays which are useful for determination of MASP-2 activity or levels in patients suffering from e.g. infections, inflammatory disorders and spontaneous recurrent abortion. The pharmaceutical composition comprising MASP-2 inhibitor is useful for treating inflammatory disorders. The present sequence is human MASP-2 protein.

Note: The present sequence is stated as being the same as SEQ ID NO:2 shown in figure 6 of the specification (AAE14564).
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                     Claim 20;
                                                                                                                                                                                                                diagnostics, forensics, responsible for genetic
                                                                                                                                                                                                                                                                                                                                                    Drmanac RT,
                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                N-PSDB; AAS85321
                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG21134 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #21125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensi-
food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      υ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ing enzyme and involved in lectin pathway of complement pharmaceutical composition comprising MASP-2 is useful
                                                                                                                                                                                                                                                                                                                  2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                 SEQ ID No 51493; 103pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     686
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                                                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                  Tang
                                                                                                                                                                                                                                                                                                                                                    YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1034 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 238;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23;
.5e-22;
s 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     forensic;
                                                                                                                                                                                                                                          mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 6
AAU87257
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Best Local
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           07-JUN-2000
28-JUN-2000
30-JUN-2000
07-JUL-2000
07-JUL-2000
11-JUL-2000
11-JUL-2000
14-JUL-2000
26-JUL-2000
26-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostics forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                            18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                            16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                            24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                           31-JAN-2000;
04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                adenocarcinoma; reproductive system disorder; testicular feminisatio endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder kidney fallure; blood disorder myocardial infarction; wound healing; cell prollferation; skin aging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Central nervous system; CNS; autoimmune disease; rheumatoid arthri hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quantitating a polypeptide in tissue, as molecular weight markers and
                                                                                                                                                                                                                                                                                                                          17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU87257 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                       WO200155318-A2
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             752 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              food supplement. (II) and its binding partners are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TPLGPKWPEPVFGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                     additive;
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2000US-0209467.
2000US-0214886.
2000US-0215135.
2000US-0216647.
2000US-0217487.
2000US-0217487.
2000US-0217496.
2000US-021963.
2000US-021963.
2000US-0220964.
2000US-0220964.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                            2000US-0198123.
2000US-0205515.
                                                                                                                                                                                                            2000US-0189874.
2000US-0190076.
                                                                                                                                                                                                                                             2000US-0186350
                                                                                                                                                                                                                                                            2000US-0184664
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2000US-0180628
                                                                                                                                                                                                                                                                                                                          2001WO-US01332
                                                                                                                                                                                                                                                                                                                                                                                                                                                   food preservative; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein #167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 238; DB 22;
Pred. No. 8.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  testicular feminisation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorder;
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2000US-022451 2000US-022521

2000US-0225268 2000US-0225470 2000US-0225447 2000US-0225757 2000US-0225758 2000US-0225759 2000US-0225759 2000US-0226681 2000US-0226681 2000US-0226681 2000US-0227189 2000US-0227189

22-AUG-2000; 23-AUG-2000;

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The invention describes an isolated nucleic acid molecule (I) encoding a convel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative clisorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. acradiac arrest, cerebrovascular disorders e.g. acradiovascular disorders angiogenesis, nervous system disorders e.g. Alzheimer's disease and amplotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system conditions of the cellular level e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2000
17-NOV-2000
                                                                                                                                                                                                                                                                                              WPI; 200
N-PSDB;
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05-DEC
05-DEC
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06-DEC
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08-DEC
                                                                                                                                                                                                                                        New isolated nucleic acid encoding a preventing, treating or ameliorating food additives or preservatives -
                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                        Rosen
                                                                                                                                                                                                                                                                                              2001-581633/65.
DB; ABK43587.
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 disorders
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2000US-0250391.
2000US-0251030.
2000US-0251988.
2000US-0256719.
2000US-0251479.
2000US-0251856.
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2000US-0246525.

2000US-0246526.

2000US-0246527.

2000US-0246528.

2000US-0246532.

2000US-0246610.

2000US-0246611.

2000US-0246611.

2000US-0246613.

2000US-0246613.

2000US-0246613.

2000US-0246613.
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2000US-0254097.
2001US-0259678.
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2000US-0251869.
2000US-0251989.
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2000US-0249209.

2000US-0249211.

2000US-0249211.

2000US-0249212.

2000US-0249213.

2000US-0249214.

2000US-0249215.

2000US-0249215.

2000US-0249215.

2000US-0249218.
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2000US-0249300
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2000US-0249245
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3-0246523
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involving
                                                                                                                                                                                                                                                                                                                                       Ruben
                                                                                                                                                                                                              837pp;
                                                                                                                                                                                                                                                                                                                                       SM.
neovascularisation
                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                     medical
                                                                                                                                                                                                                                                     for diagnosing, conditions and
 malignancies,
                                                                                                                                                                                                                                                        used
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4-SEP-2000;

2000US-0234223. 2000US-0234274. 2000US-0234997. 2000US-02354998. 2000US-0235484. 2000US-0235834. 2000US-0235834.

2000US-0233065 2000US-0233064 2000US-0232401 2000US-0232399 2000US-0232400 01-SEP-2000 05-SEP-2000 05-SEP-2000 06-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000

2000US-0230437. 2000US-0230438. 2000US-0231242. 2000US-0231243.

2000US-023124 2000US-023124

2000US-0228924. 2000US-0229287. 2000US-0229343. 2000US-0229344. 2000US-0229344. 2000US-0229345. 2000US-0229509. 2000US-0229513.

26-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 02-OCT-2000 03-OCT-2000 04-NOV-2000 08-NOV-2000 09-NOV-2000 08-NOV-2000 08-NOV-2000

2000US-0236327 2000US-0236369 2000US-0236369 2000US-0236370 2000US-0236802 2000US-0237037 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0241785 2000US-0241786 2000US-0241786 2000US-0241786 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0241809 2000US-0246474 2000US-0246474 2000US-0246474 2000US-0246475 2000US-0246477

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Best Loc
Matches
  07-JUL-2000
11-JUL-2000
11-JUL-2000
26-JUL-2000
26-JUL-2000
14-AUG-2000
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19-MAY-2000;
77-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; gene therapy; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal dipulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200154474-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA SEQ ID NO: 563.
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21; Conservative
  2000US-215135P.
2000US-216880P.
2000US-217487P.
2000US-217487P.
2000US-217964P.
2000US-229963P.
2000US-224518P.
2000US-225213P.
2000US-225214P.
2000US-225214P.
2000US-225214P.
2000US-225266P.
2000US-225276P.
2000US-22575P.
2000US-22575P.
2000US-22575P.
2000US-225758P.
2000US-225758P.
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2000US-225758P.
2000US-225759P.
2000US-225759P.
2000US-225759P.
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2000US-205515P
2000US-209467P
2000US-214886P
2000US-215135P
2000US-216647P
2000US-216880P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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Pred.
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ed. No. 0.00039;
Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorder;
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  14-SEP 2000
11-SEP 2000
21-SEP 2000
25-SEP 2000
26-SEP 2000
27-SEP 2000
29-SEP 2000
29-SEP 2000
29-SEP 2000
29-SEP 2000
29-SEP 2000
02-OCT 2000
03-OCT 2000
04-NOV 2000
06-NOV 2000
08-NOV 2000
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23-AUG-2000
30-AUG-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
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2000US-229345P
2000US-229509P
2000US-229513P
2000US-230437P
2000US-230438P
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2000US-227182P.
2000US-227009P.
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RESULT 8
AAU19914
ID AAU1
XX
AC AAU1
XX
DT 06-E
XX
DE NOVE
XX
Huma
                                                                                                                                                                                                                                                                                                        Matches
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, nuscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                              renal
is a p
                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acid n polypeptide is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
 Human; calcium-binding protein; calcium flux; neurological disease;
                                        Novel human
                                                                          06-DEC-2001
                                                                                                                                            AAU19914 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen
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17-NOV-2000;
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17-NOV-2000;
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                                                                                                                                                                                                                                                   protein of
                                                                                                                                                                                                                                PXWDSKEPVCIAACGGVIRNATTGRIVSPGFPGNYSNNLTCHWLLEAPEGQR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-476161/51.
DB; ABA06477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA,
                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                            174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barash SC,
                                      calcium-binding
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US -249208P
2000US -249211P
2000US -249211P
2000US -249213P
2000US -249214P
2000US -249218P
2000US -249218P
2000US -249218P
2000US -249218P
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2000US -250160P
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2000US -251160P
2000US -2511479P
2000US -2511856P
2000US -2511869P
                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO:
                                                                                                                                                                                                                                                                                                                                                                            AΑ;
                                                                                                                                                Protein; 174
                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                                                                                                                                                                                                                                                                                                     39.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563; 859pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    molecule encoding an inflammation-associated n preventing, treating or ameliorating a medi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben
                                      protein #23
                                                                                                                                                                                                                                                                                                  Score 93.5; DB 22;
Pred. No. 0.00039;
3; Mismatches 13;
                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                     Length 174;
                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        medical
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                    2;
   31-JAN-2000
04-FEB-2000
04-FEB-2000
01-MAR-2000
11-MAR-2000
11-MAR-2000
11-MAR-2000
07-JUN-2000
07-JUL-2000
07-JUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune dysfunction; digestive disorder; neoplastic disease;
blood disorder; infectious disease; gene therapy; immunosuppressive;
antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-2001;
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2000US-0179065.
2000US-0188628.
2000US-01886628.
2000US-01886628.
2000US-01886628.
2000US-019874.
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2000US-0216846.
2000US-0216846.
2000US-0216846.
2000US-0211680.
2000US-0211890.
2000US-021890.
2000US-021891.
2000US-0228518.
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2000US-0228566.
2000US-022856.
2000US-023854.
2000US-023854.
2000US-023854.
2000US-023854.
2000US-023856.
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B S 8X

-SEP-2

13-OCT

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20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
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20-OCT-2000;
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21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
2000US-0250391.
2000US-0251988.
2000US-0256719.
2000US-0256719.
2000US-0251479.
2000US-0251868.
2000US-0251869.
2000US-0251869.
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2000US-0234274.
2000US-0234997.
2000US-0234998.
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2000US-0249265
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2000US-0249213
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2000US-0249211
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2000US-0236369
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     DT NOS X W X E X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X P X X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X P X
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Matches 21
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11-DEC-2000;
05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represent the novel human calcium-binding proteins. Note: The sequence data for this patent did not for specification, but was obtained in electronic format ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). In novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit
                         Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activities mediated by calcium-binding proteins. The polynucleotides the invention are also useful in gene therapy. AAU19892-AAU19969
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N-PSDB; AAS31599.
                                                                                                                                                                      21-FEB-2000; 2000EP-0200610
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                                                                                                                                                                                                                                                                                                                                                                gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                           Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted
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nilarity 40.4%;
Conservative
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2000US-0254097.
2001US-0259678.
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                                                                                                                                                                                                                                                                                                                                                                expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping.
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d cDNA (AAS31577-AAS31654) and genomic
proteins. The sequences of the invention
prevention and/or prognosis of diseases
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Pred. No. 0.00039;
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                The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
                                                                   Claim 13;
                                                                                            New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedure
                                                                                                                                                                N-PSDB;
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)B; AAC01735.
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secreted proteins. The 5' polyA+ RNAs derived from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; protease; PRTS; gastrointestinal disorder; peptic esophagitis; indigestion; gastritis; cardiovascular disorder; reproductive disorder; hypertensive heart disease; myocardial infarction; autoimmune disorder; inflammatory disorder; rheumatoid arthritis; cell proliferative disorder; arteriosclerosis; cancer; epithelial disorder; eczema; endometriosis;
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17-MAR-2000;
30-MAR-2000;
14-APR-2000;
20-APR-2000;
               Claim 1;
                                polynucleotides
                                         New polypeptide for t autoimmune disorders,
                                                                    N-PSDB;
                                                                                              Hafalia A,
                                                                                                    Yue H, Lu DAM, Policky JL,
Au-Young J, Bandman O, Lal
Tang YT, Burford N, Baughn
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DB; AAH43512.
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               Page 109-11;
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; 2000US-193182P.
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                                         treating gastrointestinal, s, comprises novel human pr
             129pp; English.
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Nguyen DB,
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Yao MG, Walia
                                                cardiovascular
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                                         (PRTS)
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                                                                                                             Hillman
                                                                                                                       Khan FA;
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The

sequences

given

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AAB47559-69 show novel human proteases PRTS-1

The invention relates to a mannan-binding lectin (MBL) associated serine protease-3 (MASP-3) polypeptide. MASP-3 exerts an inhibitory effect on the complement activation particularly when bound to MBL/MASP-2 complexes and directly activates complement system through binding to MBL. The MASP-3 polypeptides, polynucleotides and modulators are useful for preparing a pharmaceutical composition for treating aberrant MASP-3 activity such as infections, cancer, MBL-deficiency, disorders of the

reproductive system diseases associated

associated with

cancer, MBL-deficiency, disorders of the ve system. The MASP-3 polypeptide is also ssociated with human immunodeficiency virus.

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RESULT 12
AAB85060
ID AAB85
Вb
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proliferative (arteriosclerosis, cancers), epithelial (neurological (Huntington's disease), and reproductive (disorders. This protein shows homology with the human P100 serine protease of Ra-reactive factor.
                                                                                                                                 Claim
                                                                                                                                                        Novel pure mannan-binding lectin associated serine protease polypeptides and polypucleotides encoding the protein, used treating reoxygenated ischemic tissues, mannon-binding lectideficiency, multiple sclerosis
                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
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                                                                                                                                                                                                                                                                  Jensenius JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiarthritic; antianemic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mannan-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human serine protease MASP-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mannan-binding lectin associated serine protease-3; MASP-3; MBL; mannan-binding lectin; complement; infection; cancer; cytostatic; immunomodulator; neuroprotective; anticonvulsive; antirheumatic;
                                                                                                                                                                                                                                                                                                         (JENS/)
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THIEL S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  These proteases can be administered in pharmaceutical compounds
                                                                                                                                Page 88-96;
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45.2%;
                                                                                                                               99pp; English.
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Pred. No. 0.
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RESULT 13
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ID AAB70
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Matches 14
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therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder (e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator cactivity or of latency or predisposition to a PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX
                                                                                                                                             The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene
                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                           Nucleic acids encoding secreted polypeptides, designated PROX polypeptides, useful for treating a syndrome associated with PROX-associated disorder, e.g. cancer - \,
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-147509/15
                                                                                                                                                                                                                                                                                                                                                                                                                   Shimkets RA,
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10-AUG-2000; 2000US-0148433
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                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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gene therapy; cell proliferation; differentiation disorder; c
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURA-) CURAGEN CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated disorder;
                                                                                                                                                                                                                                                                                                                                                             AAF74440.
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45.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gestational disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID NO:18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 728; 0.0021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pre-clampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
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                                    of.
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5 PKW--PEPV--21;

Conservative

Mismatches

13;

Indels

15;

Caps

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----FGRLASPGFPGEYANDQERRWTLTAPPGYR 41

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RESULT 14
AAB70540
ID AAB70
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Best Local
                              Query Match
                                                                                  The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder (e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX AAF74418 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding secreted polypeptides, designated PROX polypeptides, useful for treating a syndrome associated with a PROX-associated disorder, e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; PRO; PROX; cytostatic; immunomodulatory; reproduction; gene therapy; cell proliferation; differentiation disorder; cimmune associated disorder; gestational disease; pre-clampsia
                                                           Sequence
                                                                                                                                                                                                                                                                                                            Claim 1; Page 35-37; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAF74441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-AUG-1999; 99US-0148433
10-AUG-2000; 2000US-0148433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO10 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB70540;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-147509/15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-AUG-2000; 2000WO-US21857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403 PEWDSKEPVCIAACGGVIRNGTTGRIVSPGFPGNYSNNLTCHWLLEAPEGQR
                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 PKW--PEPV------FGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                 Similarity
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                                                             525
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                                                             AA;
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              38.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (F)
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            Score 91.5;
Pred. No. 0
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Pred. No. 0.0023;
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              .0023;
                              DB
                         22;
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                           Length 525;
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RESULT 15
AAB70541
ID AAB70
XX AAB70
AC AAB70
XX 09-MA
XX Human
XX Human
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                                                                                                                                                                               RESULT 16
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                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
     09-MAY-2001
                                                              AAB70542;
                                                                                                                    AAB70542 standard; Protein; 526 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder, e.g. a cell proliferation and/or differentiation disorder e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated with a PROX associated with a PROX-associated with a PROX-associ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-AUG-2000; 2000WO-US21857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROX-associated disorder, e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-AUG-2000; 2000US-0148433
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                                                                                                                                                                                                                                                               403 PFWDSKEPVCIAACGGVIRNGTTGRIVSPGFPGNYSNNLTCHWLLEAPEGQR
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                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                        PKW--PEPV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 38-40; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  525
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein sequence
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     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                     38.4%;
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                                                                                                                                                                                                                                                                                                                  -FGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                 Ψ
                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        91.5;
No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                        DB 2
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                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                               454
                                                                                                                                                                                                                                                                                                                                                                                 15;
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ID AAE1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                        AAE15854 standard;
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epilepsy; Parkinson's disease; sexual
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21; Conserv
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medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder (e.g. cancer or immune associated disorders) and a gestational disease
nootropic; neuroprotective; anticonvulsant; cerebroprotective; stroke; vasotropic; neuronal growth; growth factor-mediated chemotaxis; trauma; neurological disorder; muscular dystrophy; muscle injury; vulnerary; amyotropic lateral sclerosis; multiple sclerosis; ischaemia; diabetes;
                                                                                                                                                                                                                                                             Human; SEZ6; neural regeneration; seizure; infertility; gene therapy; stroke; Alzheimer's disease; Huntington's disease; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and antibodies are useful in the manufacture of a nucleic acids and acids acids and acids acids and acids acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human SEZ6 mature protein.
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10-AUG-2000; 2000US-0148433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO12 protein sequence SEQ ID NO:24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROX-associated disorder, e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             403 PFWDSKEPVCIAACGGVIRNGTTGRIVSPGFPGNYSNNLTCHWLLEAPEGQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 PKW--PEPV------FGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fernandes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (F)
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Pred. No. 0.0023;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunomodulatory; reproduction;
ion; differentiation disorder; cancer;
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RESULT 18
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                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              other treatment modalities which may prevent, suppress or cure a pathology or disease associated with hSEZ6 activities. SEZ6 is also useful for treating abnormal primary or secondary sexual development, e.g., impotence, infertility or reduced libido. The hSEZ6 polynucleotide is useful for treating the above mentioned disorders by gene therapy techniques. The present sequence is human SEZ6 mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease. SEZ6 is useful for treating a patient suffering from a neurological disorder such as epilepsy, Alzheimer's disease, Parkinson's disease, seizure related disorder or a disorder associated with stroke. SEZ6 DNA is useful as probes for gene mapping and for detecting transcription, translation and/or expression of hSEZ6 polypeptide in human tissue. A transgenic animal is useful as an animal model in research and drug development procedures, and for testing compounds or research and drug development procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth factor-mediated chemotaxis, altered behavioural patterns, e.g., sleep or eating disorders and for treating neurological disorders such as trigeminal neuralgia, Bell's palsy, myasthenia gravis, muscular dystrophy, muscule injury, invertebrate disk syndrome, thoracic outlet destruction syndrome, amyotropic lateral sclerosis, multiple sclerosis, ischaemia associated with stroke, neuropathy associated with diabetes, spinal cord trauma, facial nerve crush and other trauma, Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human SE26 polypeptide useful for inducing neural regeneration, inhibiting neural degeneration, preventing seizures, and for treating infertility, Alzheimer's disease, stroke, seizures, Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-082840/11.
N-PSDB; AAD25344.
   Human; SEZ6; neural stroke; Alzheimer's
                                                         Human SEZ6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    growth, neurite outgrowth, neuronal regeneration, neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated human SEZ6 (hSEZ6) polypeptide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-2000; 2000US-200200P
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                                                                                                   26-MAR-2002
                                                                                                                                                                             AAE15853 standard;
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                                                                                                                                                                                                                                                                          379
                                                                                                                                                                                                                                                                                                                                                  Local Similarity es 21; Conser
                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  corresponding DNA molecule. SEZ6
                                                                                                                                                                                                                                                                                                          PKW--PEPV------FGRLASPGFPGEYANDQERRWTLTAPPGYR 41
                                                                                                                                                                                                                                                                      PFWDSKEPVCIAACGGVIRNATTGRIVSPGFPGNYSNNLTCHWLLEAPEGQR 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 122-125; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                829 AA;
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                 (first
                                                                                                                                                                           Protein; 853
regeneration; seizure; infertility; gene therapy; disease; Huntington's disease; myasthenia gravis;
                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                  38.4%;
                                                                                                                                                                                                                                                                                                                                            Score 91.5; DE Pred. No. 0.003 3; Mismatches
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                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is useful for enhancing
                                                                                                                                                                                                                                                                                                                                                                  .0038;
                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                  13;
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                                                                                                                                                                                                                                                                                                                                                15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuronal
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Matches
                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth factor-mediated chemotaxis, altered behavioural patterns, e.g., sleep or eating disorders and for treating neurological disorders such as trigeminal neuralgia, Bell's palsy, myasthenia gravis, muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human SE26 polypeptide useful for inducing neural regeneration, inhibiting neural degeneration, preventing seizures, and for treating infertility, Alzheimer's disease, stroke, seizures, Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vasotropic; neuronal growth; growth factor-mediated chemotaxis; trauma; neurological disorder; muscular dystrophy; muscule injury; vulnerary; amyotropic lateral solerosis; multiple sclerosis; isochaemia; diabetes; epilepsy; Parkinson's disease; sexual development; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dystrophy, muscle injury, invertebrate disk syndrome, thoracic outlet destruction syndrome, amyotropic lateral sclerosis, multiple sclerosis, ischaemia associated with stroke, neuropathy associated with diabetes, spinal cord trauma, facial nerve crush and other trauma, Huntington's
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                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                         useful for treating abnormal primary or secondary sexual development, e.g., impotence, infertility or reduced libido. The hSEZ6 polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth, neurite outgrowth, neuronal regeneration,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD25344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-082840/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Su EW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               its corresponding DNA molecule. SEZ6 is useful for enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated human SEZ6 (hSEZ6) polypeptide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ELIL ) LILLY & CO ELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200183552-A2
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                                                                                                                                                                                                      techniques. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        impotence; libido.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Page 119-122; 127pp; English
                                      Similarity
                                                                                                                                                                                                                                                for treating
                                                                                                                                          853 AA;
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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25..853
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                                      38.4%;
                                                                                                                                                                                                                                                the above
Score 91.5; r
Pred. No. 0.00
3; Mismatches
                                                                                                                                                                                                      is human SEZ6 protein
                                                                                                                                                                                                                                      mentioned disorders by gene therapy
                                      .0039;
                                                                          ВG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuronal survival,
                                                                   Length 853;
   Indels
   15;
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RESULT 20
AAB70538
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ID AAB7
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Best Local
 Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated
                                Human PRO8 protein sequence SEQ ID NO:16
                                                                 09-MAY-2001
                                                                                                                                  AAB70538 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; PRO; PROX; cytostatic; immunomodulatory; reproduction; gene therapy; cell proliferation; differentiation disorder; caimmune associated disorder; gestational disease; pre-clampsia
                                                                                                                                                                                                                                                                                                                                                                         (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder. AAF774432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 24-27; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding secreted polypeptides, designated PROX polypeptides, useful for treating a syndrome associated with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimkets RA; Fernandes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-AUG-1999; 99US-0148433
10-AUG-2000; 2000US-0148433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO7 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB70537 standard; Protein; 993
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        disorder, e.g. a cell proliferation and/or differentiation disorder (e.g. cancer or immune associated disorders) and a gestational disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAF74438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROX-associated disorder, e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-AUG-2000; 2000WO-US21857.
                                                                                                                                                                                                                403 PIWDSKEPVCIAACGGVIRNATTGRIVSPGFPGNYSNNLTCHWLLEAPEGQR 454
                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                            PKW--PEPV------FGRLASPGFPGEYANDQERRWTLTAPPGYR 41
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 ₽RO;
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21; Conserv
                                                                                                                                                                                                                                                                                                                                             993
PROX; cytostatic; immunomodulatory; reproduction;
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                                                                (first entry)
                                                                                                                                  Protein; 994
                                                                                                                                                                                                                                                                                            38.4%;
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                                                                                                                                                                                                                                                                                            Score 91.5; DB 2
Pred. No. 0.0046;
                                                                                                                                AA
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                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                           Length 993;
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Search completed: January 11, Job time : 119 secs

2003, 10:48:09

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                                                                                                                                                        Query Match
Best Local Similarity
Matches 21; Conser
                                                                                                                                                                                                                                                                                                                                                                              The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder (e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 28-31; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding secreted polypeptides, designated PRO polypeptides, useful for treating a syndrome associated with
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10-AUG-2000; 2000US-0148433.
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immune associated disorder; gestational disease; pre-clampsia.
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403 PIMDSKEPVCIAACGGVIRNATTGRIVSPGFPGNYSNNLTCHWLLEAPEGQR 454
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                                                                        -FGRLASPGFPGEYANDQERRWTLTAPPGYR
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                                                                                                                                                        Score 91.5; DB 2
Pred. No. 0.0046;
3; Mismatches 1
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Command line parameters:

-WODEL-frame+_p2n.model -DEV-xlp
-Q-cgn2_1/USPTQ_spool/US09874198/runat_10012003_092043_2562/app_query.fasta_1.199
-Q-cgn2_1/USPTQ_spool/US09874198/runat_10012003_092043_2562/app_query.fasta_1.199
-DB-GenEmbl -QEMT-fastap -SUFFIX-p2n.rge -MIMMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRAMS-human40.cdi -LIST-60
-DCCALION-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-20 -MODE-LOCAL
-DUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US09874198_eCGN_1_1_3637_erunat_10012003_092043_2562 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-MARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPOP-6 -FGAPOP-6 -FGAPOXT-7
-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Maximum Match 100%
Listing first 60 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
BLOSUM62
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238
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Copyright (c) 1993 - 2003 Compugen Ltd.
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_mus:*
35: em_htg_rod:*
36: em_htg_vrt:*
37: em_htg_vrt:*
38: em_sy:*
41: em_htgo_nus:*
41: em_htgo_nus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	C 233333333002272223333333333333333333333	C 115 C 116 117 118 220	;	Result
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AC0046154 AC007920 AC072019 AC072019 AX084227 AF502130 AX084223 AX084225 AX084225 AX084225 AX084225 AX084229 AX084229 AX084229 AX084229	MMU1916 RNO18573 RNO1856 RNO1856 RNO1856 AB009072 AB0109272 AB010926 AF004661 AF004661 RNO277423 HUMMASP AB049755 AX2544423 AX156466 AF284421 D17525 MUSCRARF AC117672	MMU250369 MMU19160 MMU19163 AB009459 BC013893 AL591032 AL606969 RN0277747 AC011553 AC011553	HOSA18282 AB008047 HOSA18283 HOSA18281 HOSA18284 HSMASP2 HSMASP2PR AB033742 HOSA18287 AB033742 HOSA18287 AB0318287	ID
AC046154 Homo sapi AC007920 Homo sapi AC007920 Homo sapi AC072019 Homo sapi AX084227 Sequence AF502130 Homo sapi AX084223 Sequence AX084225 Sequence AX084225 Sequence AX084235 Sequence AX08423 Sequence AX08425 Sequence AX08425 Sequence	Y19161 Rattus Norv Y18573 Rattus Norv Y18570 Rattus Norv Y18578 Rattus Norv Y18568 Rattus Norv AB009072 Xenopus 1 AB010813 Homo sapi AF004661 Rattus no AB007603 Homo sapi AF007603 Homo sapi AB077423 Rattus no D28593 Human mRNA AB049755 Mus muscu AX254423 Sequence AX156466 Sequence AX158466 Sequence AX1586466 Sequence AX158466 Sequence AX1586466 Sequence	Mus muse Mus muse Mus muse Mus muse Mus muse Rattus Rattus		iptio

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   3'UTR
                                                                        mat_peptide
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Submitted (19-007-1998) W.J.
and, Immunology, University o
138, Leicester LEI 9HN, UK
Related sequence Y09926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structural gene
J. Immunol. 162 (6), 3481-3490 (1999)
99192764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stover,C.M., Thiel,S., Thelen,M., Lynch,N.J., Vorup-Jensen,T., Jensenius,J.C. and Schwaeble,W.J.

Two constituents of the initiation complex of the mannan-binding lectin activation pathway of complement are encoded by a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           683 bp mRNA linear PRI
Homo sapiens mRNA for mannose binding lectin-associated
protease-2, alternatively spliced transcript (clone phl-
718282
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protein; mannose binding protein; serine protease.
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 /product="mannose binding lectin-associated protease-2 related protein, MAp19 (19kDa)" /note-"alternative" 529. .683
                                                                                                                 /translation="GGSVATPLGPKWDEPVFGRLASPGFPGEYANDQERRWTLTAPPGYRLRLYFTHFDLELSHLCEYDFVKLSSGAKVLATLCGQESTDTERAPGKDTFYSLGSSLDITFRSDYSNEKPFTGFEAFYAAEDIDECQVAPGEAPTCDHHCHNHLGGFYCSCRAGYVLHRNKRTCSEQSL"
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                                                         /gene="MASP-2"
                                                                        /gene="MASP-2"
16. .525
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                                                                                                                                                                                                                                    /codon_start=1
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/note="alternative"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                           /clone="phl-7"
                                                                                                                                                                                                                                                                                                                                                                   /chromosome="
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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    Schwaeble, Department of Microbiology
of Leicester, University Road, PO Box

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n, MAp19 (19kDa)"
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AX327362 Sequence
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                                                                                                                                                                                                                                                              Direct Submission
Submitted (10-OCT-1997) Minoru Takahashi, Fukushima M College, Department of Biochemistry: 1 Hikarigaoka, F Fukushima 960-12, Japan (E-mail:minolta@cc.fmu.ac.jp. Tel:81-245-48-2111) Fax:81-245-48-2111)
Sequence update (13-Dec-1997).
                                                                                                                                                                                                                                                                                                                                                                                             Takahashi,M., Endo,Y., Fujita,T. and Matsushita,M. A truncated form of mannose-binding lectin-associated serine protease (MASP)-2 expressed by alternative polyadenylation is component of the lectin complement pathway

Int. Immunol. 11 (5), 859-863 (1999)
                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 725)
Takahashi, M., Matsushita, M. and Fujita, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                    /gene="smap"
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/codon_start=1
/product="small mBL-associated protein"
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/protein_id="BAA78616.1"
/db_xref="g1:5002494"
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/translation="mrllTlLGLLCGSVATPLGPKWPEPVFGRLASPGFPGEYANDQE
/translation="mrllTlLGLLCGSVATPLGPKWPEPVFGRLASPGFPGEYANDQE"
/translation="mrllTlLGLLSHLCEYDFYKLSSGAKVLATLCGGESTDTERAPG"
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27. .71
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27. .584
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246 c 1
/gene="smap"
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/db_xref="taxon:9606"
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Conservative:
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                                                                                                                                                                                                                              Direct Submission
Submitted (19-0CT-19981AW.J.
and, Immunorogy, University o
138, Leicester LE1 9HN, UK
                                                                                                                                                                                                                                                                                                                                                                             Stover.C.M., Thiel.S., Thelen.M., Lynch.N.J., Vorup-Jensen.T., Jensenius,J.C. and Schwaeble.W.J.

Two constituents of the initiation complex of the mannan-binding lectin activation pathway of complement are encoded by a single
                                                                                                                                                                                                                                                                                                                                                   structural gene
J. Immunol. 162 (6), 3481-3490 (1999)
                                                                                                                                                                                                                                                                                           2 (bases 1 to 729)
Schwaeble, W.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 729)
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268 c
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Jensenius,J.C. and Schwaeble,W.J.
Two constituents of the initiation complex of the mannan-binding
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Direct Submission
Submitted (19-OCT-1998) W.J.
and, Immunology, University c
138, Leicester LEI 9HN, UK
                                                                 2 (bases 1 to schwaeble, W.J.
                                                                                                                                      J. Immunol. 162
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693. .698
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protease-2 related protein, MAp19 (19kDA)"
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    Schwaeble, Department of Microbiology
of Leicester, University Road, PO Box

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         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1184)

Stover,C.M., Thiel,S., Thelen,M., Lynch,N.J., Vorup-Jensen,T., Jensenius,J.C. and Schwaeble,W.J.

Two constituents of the initiation complex of the mannan-binding
                                                                                                                                                             Y18284
                                                                                                                                                                       Homo sapiens mRNA for mannose bin protease-2, incompletely spliced
                                                                                                                    protein; mannose binding p
                                                                                           Homo sapiens
                                                                                                                                               Y18284.1 GI:5459320
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lectin activation pathway of complement are encoded by a single
                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="mannose binding lectin associated serine
protease-2 related protein, Map19 (19kDa)"
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22. .579
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/db_xref="taxon:9606"
/chromosome="1"
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Schwaeble, W. J.
Direct Submission
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99192764
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/gene="MASP-2"
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protease-2 related protein, MAp19 (19kDa)"
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/clone="ph1-8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08-JUN-1996) S. Thiel, University of Aarhus, Dept. of Medical Microbiol. & Immunol., Bartholin Building, Wilhelm Meyers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Translation="MRLITLIGLICGSVATPLGPKWPEDVFGRLASPGFPGEVANDQE
/Translation="MRLITLIGLICGSVATPLGPKKLSGAKVLATLCGQESTDTERAPG
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LQGHLPLKSFTAVCQKGGSWDRPMPAGSIVDGGPDDLLFSGKVEYITGPGVTTYKAVI
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AKPGDPFWQVLLLGGTTAAGALLYDNWYLTAAHAVYEQKHDASALDIRWGTLKRLSPH
YTQAMSEAVETHEGYTHDAGFDWDIALIKLNSKVYINSUITPTCLPRKEAESBFWTDDI
IGTASGWGLTQRGFLARNLMYVDIPIVDHQKCTAAYEKPPYPRGSVTANMLCAGLESG
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/db_xref="GI:3297879"
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/db_xref="taxon:9606"
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3'UTR
                                               sig_peptide
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Direct Submission
Submitted (08-DEC-1998) W.J. Schwaeble, Department of Immun and Microbiology, University of Leicester, University Road, Leicester LEI 9HN, UK
On Dec 13, 1998 this sequence version replaced g1:1929053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Revised by [3]
2 (bases 1 to 2455)
Thiel.S., Jensen.T.V., Stover.C.M., Schwaeble,W.:
Poulsen,K., Willis,A.C., Eggleton,P., Hansen,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (bases 1 to 2455) Schwaeble, W.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-DEC-1996) T.V. Jensen, University of Aarhus, Microbiology & Immunology, Bartholin Building, 8000 Aarhus C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2455)
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Nature 386 (6624), 506-510 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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    13, 1998 this sequence version replaced g1:1929053
Location/Qualifiers
    1. .2455

                                                                                                                                 /evidence-experimental
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/evidence=experimental
2078. . 2455
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17. .2077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene≖"MASP-2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="liver"
|...2455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Immunology
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AB033742
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Best Local Similarity:
Query Match:
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGC
                                                                                                                                                                                                                                                                        Submitted (20-007-1999) Minoru Takahashi, Fukushima Med College, Department of Biochemistry; 1 Hikarigaoka, Fukushima 960-1295, Japan (E-mail:minoita@cc.fmu.ac.jp, Tel:81-24-548-2111(ex.2232), Fax:81-24-548-6760)
                                                                                                                                                                                                                                                                                                                                                                                Takahashi,M. and Fujita,T.
Partial genomic structure of human
(MASP)-2 (from exon 1 to exon 5)
                                                                                                                                                                                                                                                                                                                                                       Published Only in DataBase (1999) 2 (bases 1 to 2819)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens sMAP, MASP2 genes for small MBL-associated protein, MBL-associated serine protease(MASP)-2, complete and partial cds. AB033742
                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                         Takahashi, M. and Fujita, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens male DNA.
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/gene="MASP-2"
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                  KDTFYSLGSSLDITFRSDYSNEKPFTGFEAFYAAEDIDECQVAPGEAPTCDHHCHNHI
                                                                                                                     /number=1
join(30. .34,116.
                                                                                                                                                                          /note="sMAP"
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                                                                                                                                                                                                                                                                ocation/Qualifiers
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Stover, C.M.,
    Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 4464)
Stover, C.M., Thiel, S., Thelen,
                                                                             lectin-associated protein; mannose binding lectin-associated protein; mannose binding protein; serine protease.
                                                                                                                                HOSA18286 4464 bp
Homo sapiens partial MASP-2 gene
                                                      Homo sapiens
                                                                                                        Y18286.1 GI:5459322
                                                                   Homo sapiens.
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/gene="MASP2"
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RRWTLTAPPGYRLRLYFTHFDLELSHLCEYDFVKLSSGAKVLATLCGQESTDTERAPG
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|693. .1824
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    Thelen, M., Lynch, N.J., Vorup-Jensen, T.,
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                            Craniata; Vertebrata; Catarrhini; Hominidae;
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                              Hominidae;
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                                          Euteleostomi;
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SOURCE

VERSION

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 4464)
Schwaeble, W.J.
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Two constituents of the initiation complex of the mannan-binding lectin activation pathway of complement are encoded by a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structural gene
J. Immunol. 162 (6), 3481-3490 (1999)
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       938
                                                                                                                                                                                                                                                                                                                                                                                              /translation="MRLLTLLGLLCGSVATPLGPKWPEPVFGRLASPGFPGEYANDQE
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GGFYCSCRAGYVLHRNKTTCSALCSGQVFTQRSGELSSPEYPRPYKLSSCTYSISLE
EGFSVILDFVESFDVETHPETLCPYDFLKIQTDREEHGPFCGKTLPHRIETKSNTVTI
TFVTDESGDHTGKKIHYTSTAHACPYPMAPPNGHVSPVQAKYILKDSFSITCETGYEL
LQGHLPLKSFTAVCQKDGSWDRPMPATVDCGPPDDLCSPSGRVEYITGBCYTTYKAVI
QYSCEETFYTMKVNDGKYVCEADGFWTSSKGEKSLPVCEPVCGLSARTTGGRTYGGQK
AKPGDDFWQVLGGTTAAGALLILYDNWYLTAAHAVYEQKHDASALDIRMCTLKRLSPH
YTQAWSEAVFIHEGYTHDAGFDNDIALIKLNKKYVINSNITPICLPRKEAESFMRTDD
IGTASGWGLTQRGFLARNLMYVDIPIVDHQKCTAAYEKPPYPRGSYTANMLCAGLESG
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     a
                                     /note="c"
2926. .4464
/gene="MASP-2"
                                                                                                                                                                                    GGFYCSCRAGYVLHRNKRTCSEQSL"
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/gene="MASP-2"
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/gene="MASP-2"
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/gene="MASP-2"
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|. .4464
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                                                                                          gene="MASP-2"
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1 (bases 1 to 4465)
Stover, C.M., Thiele, Thelen, M., Lynch, N.J., Vorup-Jensen, T., Jensenius, J.C. and Schwaeble, W.J.

Two constituents of the initiation complex of the mannan-binding lection activation pathway of complement are encoded by a single
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (19-OCT-1998) W.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
                                                                                                                                                                     Join(1. .559,2415.
/gene="MASP-2"
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                                                                                                          /gene="MASP-2"
                                                                                                                                            join(1. .559,1004.
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                                                                           oin(16.
                                                                                          'note="a"
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Indels:
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4900)
                                                                                                                                                                                  AF321558
                                                                                                                                                                                           4900 bp DNA linear PRI 18-JAN-2001 Homo.sapiens MBL-associated serine protease 2 (MASP2) gene, exons 1 through 6; and MBL-associated protein MAp19 (MASP2) gene, complete cds, alternatively spliced.
                                                                                              Homo sapiens.
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/gene="MASP-2"
/note="d"
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LQGHLPLKSFTAVCQKIGSWDRRMPAIVDCGPDDLCSSSGRVEITTGRGVTTYKAVI

OYSCEETFYMKVNDGKYVCEADGFWTSKGEKSLPVCEPVGGLSARTTGRGTYTGGKY

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IGTASGWGLTQRGFLARHLMYVDIPJVDHKCTAAYEKPPYPRGSYTAMMLCAGLESG

GKDSCRGDSGGALVFLDSETERWFVGGIVSWGSMNCGEAGQYGVYTKVINYIPWIENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MRLLTLLGLLCGSVATPLGPKWPEPVFGRLASPGFPGEYANDQE RWTLTAPPGYKLRLYETHFDLELSHLCEYDFVKLSSGAKVLATTLCGQDESTDTERAPG KDTFYSLGSSLDITFKSDYSNBKKPFTGFEAFYAAEDLDECQVAPGEAPTCDHHCHHL GGFYCSGRAGYVLHRNKRTCSALCSGOYFTQRSGELSSPEYPRYPKLSSCTYSTSLE EGFSVILDFVESFDVETHPETLCPYDFLKIQTTDREEHGPFCGKTLPHRIETKSNTVTI
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KDTFYSLGSSLDITFRSDYSNEKPFTGFEAFYAAEDIDECQVAPGEAPTCDHHCHNHL
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/note="c"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. This sequence is the entire insert of clone RP4-635E18 The true left end of clone RP4-576K7 is at 5257 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw:, SWISSPROT: Tr:, TREMBL: Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl
http://www.sanger.ac.uk/HGP/Chrl
RP4-635E18 is from the library RPCI-4 constructed by the group Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 15, 2002 this sequence version replaced gi:11967852.
During sequence assembly data is compared from overlapping clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13-JAN-2002) Wellcome Trust Sanger Institute, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
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Stover, C.M., Thiel, S., Lynch, N.J. and Schwaeble, W.J.
The rat and mouse homologues of MASP-2 and MAp19, components of the lectin activation pathway of complement lectin activation pathway of complement Immunol. 163 (12), 6848-6859 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (20-OCT-1999). Stover C.M., Dept. of Experime Immunology, University of Marburg, Deutschhausstrasse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stover, C.M.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus mRNA for mannose
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                               function="unknown"
                                                                                                                         /gene="MASP-2/MAp19"
                                                                                                                                                                                                                             /gene="mouse MAp19"
                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/variety="C57Bl6"
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                                                                                      'gene="MASP-2/MAp19"
                                                                                                                                                                                    gene="mouse MAp19"
                                                                                                                                                                     function="unknown"
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RESULT 14
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                                                                                   Submitted (13-JUL-1999) W.J. Schwaeble, Department of Immunology, University of Leicester, University Road,, Leicester LE1 9HN, UK Location/Qualifiers
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Mus musculus mRNA for mannose
Mrotease-2 related protein, M
                                                                                                                                Direct
                                                                                                                                            2 (bases 1 to 817)
Schwaeble, W.J.
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The rat and mouse homologues of MASP-2 and MAp19, components
lectin activation pathway of complement
J. Immunol. 163 (12), 6848-6859 (1999)
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammaalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 817)
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                       /organism="Mus musculus"
/strain="C57BL/6 x CBA"
/db_xref="taxon:10090"
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590. .733
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/gene="MAp19"
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Stover, C.M., Thiel, S., Lynch, N.J. and Schwaeble, W.J. The rat and mouse homologues of MASP-2 and MAP19, collectin activation pathway of complement J. Immunol. 163 (12), 6848-6859 (1999)
                                                                                                                                                                                                                                                                                                                                                         MMU19163 1145 bp mRNA line Mus musculus partial mRNA for mannose binding serine protease-2 (MASP-2 gene).
                                                                          Submitted (13-JUL-1999) W.J. University of Leicester, Univ
                                                                                                                     2 (bases 1 to 1145)
Schwaeble, W.J.
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/gene="MAp19"
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/strain="B6CBAF1/J"
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75. .647
                                                       Location/Qualifiers
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-874-198-1 (1-41) x MMU19163 (1-1145)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
            FEATURES
                                                                                                        REFERENCE
                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                    RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
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                                                                                                                                                                                                                                                           SOURCE
                                                                            AUTHORS
TITLE
                                                                                                                     MEDLINE
                                                                                                                                  JOURNAL
                                                                                                                                                             TITLE
                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                           ORGANISM
                                                                 JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                        41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                CGC 227
                                                                                                                                                                                                                                                                                                                                                                                                                        Arg 41
                                                                                                                                                                                                                                           AB009459
AB009459.1 GI:3928516
mannose-binding lectin associated serine protease-2.
Mus musculus (strain:BALB/c) 8 weeks liver cDNA to mRNA.
                     Submitted (04-DEC-1997) Minoru Takahashi, Fukushima Medical College, Department of Biochemistry: I Hikarigaoka, Fukushi Fukushima 960-1295, Japan (E-mail:minolta@cc.fmu.ac.jp, Tel:81-24-548-2111, Fax:81-24-548-6760)
                                                                                                                                                         Endo,Y., Takahashi,M., Nakao,M., Sai
Matsushita,M., Nonaka,M. and Fujita,
Two lineages of mannose-binding lect
                                                                                                                                                                                                                                                                                                           Mus musculus Masp-2
serine protease-2,
                                                                            Direct Submission
                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                       AB009459
                                                                                       Takahashi, M., Fujita, T.,
                                                                                                                     99008558
                                                                                                                                             (MASP) in vertebrates
                                                                                                       (bases 1 to 2090)
                                                                                                                                                                                                     (sites)
                                                                                                                                 Immunol. 161 (9),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="Cab65250.1"
/protein_id="Cab65250.1"
/db_xref="GI:6688733"
/translation="M5LPCPQ/LIFLGLLWSLVATILGSKWPEPVFGRLVSPGFPEKY
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ADHQDRSWTLTAPPGYRLRLYFTHFDLELSYRCEYDFVKLSSGTKVLATLCGQESTDT
EQAPGROTFYSLGPSLKVTFHSDYSNEKPTTGFEAFYAAEDVDECRVSLGDSVPCDHY
CHNYLGGYYCSCRAGYVLHQNKHTCSALCSGQVFTGKSGYLSSPEYPQPYPKLSSCTY
SIRLEDGFSVILDFVESFDVETHPEAQCPYDSLKIQTDKGEHGPFCGKTLPPRIETDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HKVTITFATDESGNHTGWKIHYTSTARPCPDPTAPPNGSISPVQAIYVLKDRFYVFCK TGFELLQGSVPLKSFTAVCQKDGSWDRPMPECS" 45. . . 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="mannose binding protease-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="MASP-2"
345 c 21
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45. .>1145
         Location/Qualifiers
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/codon_start=1
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183.00
85.37%
78.05%
76.89%
                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                           2090 bp mRNA li
2 mRNA for mannose-binding
complete cds.
                                                                                                                                 4924-4930 (1998)
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                                                                                       Endo, Y. and Matsushita, M.
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                             Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256
                                                                                                                                                          lectin-associated serine
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                                                                                                                                                                                                                                                                                                                                       linear
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                                                 Fukushima,
                                                                                                                                                                                                               Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                         associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164
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BC013893
LOCUS
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                                                             TITLE
JOURNAL
                                                                                       AUTHORS
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REMARK
COMMENT
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ORGANISM
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Best Local Similari
                                                                                                                                                                                                                                                                                                                                                              DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arg 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity:
                                                        Direct Submission
Submitted (07-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                 3070 bp mRNA linear RC Mus musculus, Similar to mannan-binding lectin serine clone MGC:13718 IMAGE:4211293, mRNA, complete cds. BC013893
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                   Strausberg, R.
                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                            Mammalia;
                                                                                                                                                                                                               Eukaryota;
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                                                                                                                                                                                                                                                                                                  BC013893.1
                                                                                                                                                                                                                                                        house mouse
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                                                                                                                                                                karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 3070)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522
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DGFSYILDFYESEDVETHPEAGCPYDSLKIQTDKGEHGPFCGKTLPPR.ETDSHKYTI
TFATDESGHITGWKLHYTSTARPCPDDTAPPNGSISFYOATYVLKDRFSVECKTGFEL
LQGSVPLKSFTAYCQKDGSWDRPMPECSIIDCGPPDDLPNGHYDYITGPOVTTYKAVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mrlliflGllwslvaTllgskwpEpvfGrlvspGfpekyaDHQD
RSWTLTAPPGYRLRLYFTHFDLELSYRCEYDFVKLSSGTKVLATLCGQESTDTEQAPG
NDTFYSLGPSLKVTFHSDYSNEKPFTGFEAFYAAEDVDECRVSLGDSVPCDHYCHNYL
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KPGDFPWQVLLLGQTTAAAGALIHDNWYLTAAHAVYEKRMAASSLNIRMGILKRLSPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTVAGWGLTQKGLLARNLMFVDIP1ADHQKCTTVYEKLYPGVRVSANMLCAGLETGG
KDSCRGDSGGALVFLDNETQRWFVGGIVSWGSINCGAAGQYGVYTKVINYIPWNENII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTQAWPEEIFIHEGYTHGAGFONDIALIKLKNKVTINGSIMPVCLPRKEAASLMRTDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAA34674.1"
/db_xref="GI:3928517"
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33. .2090
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/tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="mannose-binding lectin associated
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183.00
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78.05%
76.89%
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Matches:
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BASE COUNT
ORIGIN
                                               RESULT 18
AL591032
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  LOCUS
DEFINITION
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Local Similarity:
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                                                                                                                                                                                                                                                                                                                 41
                                                                                                                                                                                                                                                                      21
                                                                                                                                                                                                                   CCAGAGAAGTATGCTGACCATCAAGATCGATCCTGGACACTGCACTGCACCCCCTGGCTAC 181
                                                                                                                           CGC 184
                                                                                                                                                                      Arg 41
                                                                                                                                                                                                                                                                   ProGlyGluTyrAlaAsnAspGlnGluArgArgTrpThrLeuThrAlaProProGlyTyr 40
AL591032 205573 bp DNA linear ROD 14-MAR-2002 Mouse DNA sequence from clone RP22-211A10 on chromosome 4, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Series: IRAK Plate: 18 Row: n Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 675.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                           AL591032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.E.
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KPGDFPWQVLLLGQTTAAAGALIHDNWVLTAAHAVYEKRMAASSLNIRMGILKRLSPH
YTQAWPEEIFIHEGYTHGAGFDNDIALIKLKNKVTINGSIMPVCLPRKEAASLMRTDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGYYCSCRACYVLHONKHTCSALCSGOVFTGRGGYLSSPEYPOPYPKLSSCTYSIRLE
DGFSVLLDFVESFDVETHPEAGCPYDSLKIQTDKGEHGPFCKKTLPPRIETDSKHVTI
TFATDESGNHTGWKHYSTARPCPDDTAPPNGSISPVOAIVYLKDRFSVFCKTGSFKVI
LDGSVPLKSETAVCQKDGSWDRPMPECSIIDCGPPDDLPNGHVDYITGPEVTTYKAVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mRLLIFLGLLWSLVATLLGSKWPEPVFGRLVSPGFPEKYADHQD
RSWTLTAPPGYRLRLYFTHFDLELSYRCEYDFVKLSSGTKVLATLCGQESTDTEQAPG
NDTFYSLGPSLKVTFHSDYSNEKPFTGFEAFYAAEDVDECRVSLGDSVPCDHYCHNYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDSCRGDSGGALVFLDNETQRWFVGGIVSWGSINCGAADQYGVYTKVINYIPWIENII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Similar to mannan-binding lectin serine protease
2"
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17. .2074
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/tissue_type="Liver, normal. 5 mc/clone_lib="NCI_CGAP_Li9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /map="FVB/N"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAH13893.1"
/db_xref="GI:15530225"
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CGC 89937
                                                                                                                                      ProGlyGluTyrAlaAsnAspGlnGluArgArgTrpThrLeuThrAlaProProGlyTyr 40
                                                                                                                                                                                        ACACTTCTGGGTTCAAAGTGGCCTGAACCTGTATTCGGGCGCCCTGGTGTCCCCTGGCTTC
                                          Arg 41
                                                                                            Similarity:
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers abbreviations are used to associate primary accession numbers in the feature table with their source databases: Em:, EMBL; Sw:, SMISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
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AL591032
AL591032.19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP22-211A10 from the RPCI-22 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    corresponding to the overlapping clone, as we submit sequences with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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be approximately 160bp by restriction digest data."
a 50972 c 49570 g 51844 t
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180212
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Sequencing vector: M13; M77815; 0% of reads
Sequencing vector: plasmid; L08752; 99% of reads
Chemistry: Dye-terminator; 6% of reads
Chemistry: Dye-terminator Big Dye; 93% of reads
Chemistry: Dye-terminator Big Dye; 93% of reads
Consensus quality: 224154 bases at least Q40
Consensus quality: 224173 bases at least Q20
Consensus quality: 224186 bases at least Q20
Insert size: 224212; sum-of-contigs
Insert size: 224212; sum-of-contigs
Ouality coverage: 20.42x in Q20 bases; sum-of-contigs
Coverage: 21.08x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Aug 15, 2002 this sequence version replaced g1:22204261.
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Mus musculus chromosome 4 clone RP23-331P21,
PROGRESS ***, 2 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Wellcome Trust Sanger Institute
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 224312)
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178013 178112: gap of 100 bp
178113 224312: contig of 46200 bp in length.
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                                                                                                                                                                    /note="assembly_fragment:01204
fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                               /clone="RP23-331P21"
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/db_xref="taxon:10090"
/chromosome="4"
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L, *** SEQUENCING IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-MAY-2000) Wallis R., Department of Biochemistry, Glycobiology Institute, University of Oxford, South Parks Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interaction of mannose-binding protein with associated serine proteases: effects of naturally occurring mutations J. Biol. Chem. 275 (40), 30962-30969 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus partial mRNA for mannose-binding associated serine protease-2 (masp-2 gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wallis, R. and Dodd, R.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mannose-binding protein associated serine protease-2; MASP-2 gene.
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/gene="masp-2"

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Query Match:
DB:
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Search completed: January 11, 2003, 12:10:20 Job time: 3228 secs
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                                                                                                     /product="mannose-binding protein associated serine protease-2" 516\ a\ 544\ c\ 507\ g\ 470\ t .
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Conservative:
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Perfect score:
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                                                                                                                                         Score
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US-09-9808-352-14174
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Sequence 21, Appl Sequence 17, Appl Sequence 18, Appl Sequence 15, Appl Sequence 15, Appl Sequence 1712, Appl Sequence 1712, Appl Sequence 2296, Appl Sequence 2297, Appl Sequence 2297, Appl Sequence 1911, Appl Sequence 1911, Appl Sequence 1915, Appl Sequence 1915, Appl Sequence 1916, Appl Sequence 1916, Appl Sequence 1917, Appl Sequence 1917, Appl Sequence 1917, Appl Sequence 1918, Appl Sequence 1918, Appl Sequence 1917, Appl Sequence 1918, Appl Sequence 1923, A
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## ALIGNMENTS

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Sequence 3, Appli
Sequence 3, Appli
Sequence 143, App
Sequence 1924, Ap
Sequence 3, Application US/09874198
Patent NO. US20020082208A1
GENERAL INFORMATION:
APPLICANT: Jensenius, Jens Chr.
APPLICANT: Thiel, Steffen
TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING EN:
TITLE OF INVENTION: USES FOR IT
FILE REFERENCE: 99011-002002
CURRENT APPLICATION NUMBER: US/09/874,198
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/054,218
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PRIOR APPLICATION NUMBER: 60/042,678 PRIOR FILING DATE: 1997-04-03 NUMBER OF SEQ ID NOS: 8

FILING DATE: 1998-04-02

SOFTWARE: FastSEQ for Windows Version

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US-09-874-198-1 (1-41) x US-09-874-238-3 (1-2475)
                                                                                                                                  Alignment Scores:
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GENERAL THEODERS
                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2475
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                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MASP-2 COMPLEMENT-FIXING ENZYME, AND TITLE OF INVENTION: USES FOR IT FILE REFERENCE: 09011-002003 CURRENT APPLICATION NUMBER: US/09/874,238 CURRENT FILING DATE: 2001-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jensenius, Jens Chr. APPLICANT: Thiel, Steffen
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 8
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TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LOCATION: (37
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LOCATION: (37
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                                                                                                                                                                                                                                                                                                                                            OR APPLICATION NUMBER: 09/054,218
OR FILING DATE: 1998-04-02
OR APPLICATION NUMBER: 60/042,678
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Best Local Similarity:
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                                                                                                                                   Sequence 1924, Application US/09833381
Patent No. US20020132090A1
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090A1e1 Nucleic Acid and Protein Homologs
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
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SEQ ID NO 143
LENGTH: 810
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APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06
                                                               NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1924
LENGTH: 742
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CURRENT FILING DATE: 2001-01-17
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NAME/KEY: misc_feature
                  FEATURE:
                                ORGANISM: Homo sapiens
                                                    TYPE: DNA
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; OTHER INFORMATION: n - A,T,C
US-09-833-381-1924
RESULT 6
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CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 21
LENGTH: 1988
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APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
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CATION: (178)..(1752)
004-551-21
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; LOCATION: (178)...(1752)
; OTHER INFORMATION: n 2077 can be
US-10-004-551-19
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; LOCATION: (178)..(1752)
; OTHER INFORMATION: n 2077 can be
US-10-004-551-17
Alignment Scores: Pred. No.:
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Publication No. US20030004310A1
GENERAL INFORMATION:
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SEQ ID NO 17
LENGTH: 2127
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APPLICANT: FERNANDES, ELMA
APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/004,551
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
                                                                                                                                                                                                                                                                                                                            APPLICANT: SHIMKETS, RICHARD A
APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: 15966-559
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PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
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CURRENT FILING DATE: 2001-12-05
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                                                                                                                                                           LENGTH: 2127
TYPE: DNA
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US-10-004-551-13
Sequence 13, Application US/10004551
Publication No. US20030004310A1
GENERAL INFORMATION:
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LENGTH: 2143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/004,551 CURRENT FILING DATE: 2001-12-05 PRIOR APPLICATION NUMBER: 09/635,949 PRIOR EILING DATE: 2000-08-10 NUMBER OF SEQ ID NOS: 110 SOFTWARE: Patentin Ver. 2.1
APPLICANT: SHIMKETS, RICHARD A
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APPLICANT: FERNANDES, ELMA
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (178)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                      1504
                                                                                                                                                                                                                                                       1384 CCCTTCTGGGATTCAAAGGAGCCCGTCTGCATCGCTGCTTGCGGCGGAGTGATCCGCAAT 1443
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004-551-23
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Match:
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; OTHER INFORMATION: n 1755
US-10-004-551-13
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; LOCATION: (178)..(3159)
; OTHER INFORMATION: n 1755
US-10-004-551-15
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Best Local Similarity:
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Query Match:
                                                                                           Alignment
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SEQ ID NO 15
LENGTH: 3879
TYPE: DNA
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LENGTH: 3863
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CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 15966-559
CURRENT APPLICATION NUMBER: US/10/004,551
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR APPLICATION NUMBER: 09/635,949
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 110
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                  Match:
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0.0296
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Conservative:
Mismatches:
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Conservative:
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US-09-917-800A-1712
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                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                           Alignment Scores
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                                                                                                                                                                                                                          Best Local Similarity:
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                                                                                                                                                                                                                                            Percent Similarity:
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OR FILING DATE: 2001-07-09
BER OF SEQ ID NOS: 1740
SEQ ID NO 1712
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CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
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                                          2566 GGTCCAGTTTGGACAAGTCCTCCTTTTGTAAACTATACTTGTGGAGGTTTCCTGACTGGA 2625
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13 -----GlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArg 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/295,798 FILING DATE: 2001-06-06 APPLICATION NUMBER: US 60/297,457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/290,645 FILING DATE: 2001-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/292,336
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Castle, Arthur
Elashoff, Michael
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31.37%
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Matches:
Conservative:
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Indels:
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; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Homo s
US-09-919-497-39
    Alignment Scores: Pred. No.:
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US-09-919-497-39
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US-09-925-302-168
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application U Patent No. US20020106662A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 168
LENGTH: 1148
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                       SOFTWARE: Pa
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REEEROE: PAIO4
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/919,497 CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                        PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/221,735 PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER FILE REFERENCE: B0801/7225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (1076)
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                                                                                                                                                         PatentIn version 3.0
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                                                RESULT 15
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LENGTH: 1480
TYPE: DNA
Sequence 92, Application US/09808602 Patent No. US20020155115A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-WO CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 3950
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Local Similarity:
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                                                                                                         ThrAlaProProGly 39
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                    Alignment Scores: Pred. No.:
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                                                                                                                                                SEQ ID NO 2256
LENGTH: 2493
TYPE: DNA
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                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14 PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14 PRIOR APPLICATION NUMBER: US 60/237,054 PRIOR FILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 3950
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CURRENT FILLING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
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TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec Acids Encoding
FILE REFERENCE: 15966-697 CIP
                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Gene Expression Profiles FILE REFERENCE: 44921-5028-WO
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OTHER INFORMATION:
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TYPE: DNA
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Shimkets, Richard
Herrman, John L
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Mezes, Peter S
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1003386CB1
US-10-044-090-613
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Best Local Similarity:
                             GEMERAL INFORMATION:

APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NO3: 15112
SEQ ID NO 3224
LENGTH: 354
TYPEF. NAS
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CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 613
LENGTH: 2555
                                                                                                                                                                                                                                                                                                   Sequence 3224, Application US/09960352 Patent No. US20020137139A1
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TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
                    TYPE: DNA
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ORGANISM: Bos taurus
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US-09-960-352-10119
Sequence 10119, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Negappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 8661
LENGTH: 392
TYPE: DNA
CORDANIES. BOG TAXELED
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
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OTHER INFORMATION: Clone ID:
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Conservative:
Mismatches:
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US-08-991-408-1
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                                                                                           US-0,9-874-198-1 (1-41) x US-08-991-408-1 (1-5145)
                                                                                                                                     Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/034
FILING DATE: 02-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,03
                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
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APPLICANT:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN CA
                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 610-407-0700
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                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 610-407-0701
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TELEX: 846169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/991,408
                                                              GlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArgArgTrp 32
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Query Match:
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Search completed: January 11, 2003, 12:47:57
Job time : 83 secs
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LENGTH: 5145
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APPLICANT: WILLETTE, ROBERT N.
APPLICANT: ELSHOURBAGY, NABIL A.
APPLICANT: LI, XIAOTONG
TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN
FILE REFERENCE: ATG-50038-D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/432,473
CURRENT FILING DATE: 1999-11-01
EARLIER APPLICATION NUMBER: 08/991,408
EARLIER FILING DATE: 1997-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0
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Indels:
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Matches:
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                Alignment Scores:
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   Pred. No.:
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Best Local Similarity:
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 3919 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 608-251-5000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
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ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 370
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                  OTHER INFORMATION:
                                                                                                                                 ORGANISM:
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CLASSIFICATION:
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Length:
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Percent Similarity:
Best Local Similarity:
Query Match:
US-09-874-198-1 (1-41) x US-09-240-473-4 (1-3919)
                                                                                                                                                         US-09-240-473-4
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US-09-240-473-4
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Query Match:
                                                                                                             Pred. No.:
                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                            TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Hom
                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hoffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3054 GAAATCAGCGCCACTCCCGGCCACCGA 3080
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                                                                                                                                                                       LOCATION: 648..36 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 53703
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                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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Matches:
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Indels:
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TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:

PROTEIN

HUMAN CARDIAC/BRAIN TOLLOID-LIKE

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Query Match:
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Best Local Similarity:
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                                                                                             GENERAL INFORMATION:
APPLICANT: ARLETH, ANTHONY J.
APPLICANT: WILLETTE, ROBERT N.
APPLICANT: WILLETTE, ROBERT N.
APPLICANT: LISTONG
APPLICANT: LISTONG
TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE PROTEIN
FILE REFERENCE: ATG-50038-D1
                                                                                                                                                                                                                                                       Sequence 3, Application US/09432473 Patent No. 6365715
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CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION UMBER: 60/034,471

PILING DATE: 02-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F

REGISTRATION NUMBER: 23,031

REFERENCE/OOCKET NUMBER: ATG-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700

TELEFAX: 610-407-0701
CURRENT APPLICATION NUMBER: US/09/432,473 CURRENT FILING DATE: 1999-11-01 EARLIER APPLICATION NUMBER: 08/991,408 EARLIER FILING DATE: 1997-12-16 EARLIER APPLICATION NUMBER: 60/034,471
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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LENGTH: 3690 base pair
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MEDIUM TYPE: Diskett
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ADDRESSEE: RATNER & PRESTIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08866650 Patent No. 5939321 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER FILING DATE: 1997-01-02 NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                 TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: DNA
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 370
                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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APPLICANT: Takahara, Kazuhiko
APPLICANT: Hoffman, Guy G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1203 GAAATCAGCGCCACTCCTGGCCACCGA 1229
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                                                   FEATURE:
                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Mammalian Tolloid-Like Protein
                                                                                                                                                    TYPE: n
                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1 Soul
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                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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ZIP: 53703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Quartes a Landau Street
LOCATION: 648..3689
OTHER INFORMATION: ,
                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                                                                      TOPOLOGY:
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SYSTEM: PC-DOS/MS-DOS
                                                                 Homo sapiens
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                                                                                                    DNA (genomic)
                                                                                                                                    double
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/product= "human mTll protein"
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Conservative:
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Best Local Similarity:
Query Match:
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US-08-377-292-1
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Sequence 3, Application US/08872757 Patent No. 6258584 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: STONE,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
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                                                                                                     1887 CAGCTGGTGGCCCCCACCCAGTACCGC 1913
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MOLECULE TYPE:
-377-292-1
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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CITY: Cincinnati
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                                                                                                                                                                                                                                                                                                                                                                   NO . .
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                                                                                                                                                                                           13 GlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArgArgTrp 32
                                                                                                                         33 ThrLeuThrAlaProProGlyTyrArg 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08 FILING DATE: 23-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Corstanje, Brahm J. REGISTRATION NUMBER: 34,804
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69.00
58.62%
44.83%
28.99%
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Matches:
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US-08-991-408-3
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Query Match:
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                                                              Sequence 3, Application US/08991408 Patent No. 6008017 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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              APPLICANT:
                                                APPLICANT:
                                                                                                                                                                                                                                          2266
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TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
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APPLICANT:
APPLICANT:
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NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,
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APPLICATION NUMBER: US/0
FILING DATE: 01-MAR-1996
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APPLICANT:
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STREET: 1155 Avenue of the Americas
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                                                                                                                                                                                                    ThrLeuThrAlaProProGlyTyrArg 41
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            WILLETTE, ROBERT N. ELSHOURBAGY, NABIL A.
                                                ARLETH, ANTHONY J.
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10-JUN-1997
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34.48%
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RECOMBINANT C-PROTEINASE AND
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Indels:
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            Percent Similarity:
Best Local Similarity:
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US-08-611-729A-7
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US-08-611-729A-7/c
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                                                                                          Alignment Scores:
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 733
ELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICATION NUMBER: US,
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                             LENGTH: 4483 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                         (212) 869-9741/8864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mann, Robert
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332..4102
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                                                                                                                                                                                                  linear
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               44.7
70.00
53.85%
46.15%
29.41%
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Gaps:
                                                            Length: Matches:
                              Mismatches:
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                 Indels:
                                               Conservative:
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-872-757-1
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                                               US-09-874-198-1 (1-41) x US-08-872-757-1 (1-2457)
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                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,22
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                 NO . .
13 GlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArgArgTrp 32
                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 415-854-36
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 10-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProLeuGlyProLysTrpProGluProValPheGlyArgLeuAlaSerProGlyPhePro 21
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                                                                                                                                                                                                                                                                                                                                             2457 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sieron, Aleksander
VENTION: RECOMBINANT C-PROTEINASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hojima,
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                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/872,757
10-JUN-1997
                                                                                                                                                                                                                                                                                                              double
                                                                                 30.1
69.00
58.62%
44.83%
28.99%
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                                                                                                                                             Length:
Matches:
                                                                                               Mismatches:
Indels:
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

us/08/839,008

OPERATING SYSTEM: SOFTWARE: Patent!

IBM PC compatible SYSTEM: PC-DOS/MS-DOS PatentIn Release #1.0, Version #1.25

COMPUTER:

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Query Match:
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                                                                                                                                       NUMBER PALES
SOFTWARE: PALES
SEQ ID NO 4
SEQ ID NO 3955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09214278 Patent No. 6291210
                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/214,278
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                         APPLICANT: Sakano, Seiji
APPLICANT: Itoh, Akira
TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/563,697
EILING DATE: 28 NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50384
                                                                                                                               LENGTH: 39
                               LOCATION: (12)..(3725)
NAME/KEY: sig_peptide
LOCATION: (12)..(89)
NAME/KEY: mat_peptide
LOCATION: (90)..(3725)
                                                                                                             ORGANISM: Homo sapiens
                                                               LOCATION:
                                                                                  NAME/KEY:
                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 1
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No . :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 GTGGCAAGTGAGGGTTTCCCCCAACCTCTACCCCCCAAACAAGAAGTGCATCTGGACAATT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1506 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                        242 ACGGTGCCCGAGGGG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 CCCAACTACACGAGACCTGTGTTCCTGTGCGGAGGGGACCGTGACCGGGGAGTCAGGTTAC 181
                                                                                                                                                                                                                                                                                                                                                            214-278-4/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProLysTrpProGluProValPhe-----
                                                                                CDS
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N: 435
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74.00
48.89%
35.56%
31.09%
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Indels:
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16
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Percent Similarity:
Best Local Similarity:
Query Match:
                                    Score:
                                                     Pred. No.:
                                                                       Alignment Scores:
                                                                                                        US-08-400-159-7
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 Best Local Similarity:
                Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Ish-Ho
APPLICANT: Henriq
                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIF: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PLOCATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1795 GGCCCC---GCGTCTGACCCGCAGCCATCGATCACTCTGCAGGCCCCCGCCAGGGCAC 1742
                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 73
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1840 CCATGGGGGCCACACACGCCGGAG-------GCTGCTGCTGCTGCCAGGCATCCCA 1796
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                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/400,159 FILING DATE: 07-MAR-1995
                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 GlyGluTyrAlaAsnAspGlnGluArgArgTrpThrLeuThrAlaProProGlyTyr 40
                                                                                                                                                                                             LENGTH: 4464 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                          nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                   : (212) 790-9090
(212) 869-9741/8864
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Lewis, Julian H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mann, Robert S
Gray, Grace E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myat, Anna M.
Fleming, Robert J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Artavanis-Tsakonas, Spyridon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pennie & Edmonds
                                                                                                                                                            double
44.5
70.00
53.85%
46.15%
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46.15%
29.41%
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                                  Length:
Matches:
                Conservative:
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Matches:
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Indels:
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R FILING DATE: 1997-08-18
R APPLICATION NUMBER: 60/0!
R FILING DATE: 1997-08-18
R APPLICATION NUMBER: 60/0!
R FILING DATE: 1997-08-18

60/056,360 60/055,684

APPLICATION NUMBER: 60/055,964

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Percent Similarity:
Best Local Similarity:
Query Match:
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; LOCATION: (642)
; OTHER INFORMATION: n
US-09-227-357-37
                                                                                                                                                                                                                                                                                                                                                          US-08-839-008-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-874-198-1 (1-41) x US-09-227-357-37 (1-985)
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EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08839008 Patent No. 5916758 GENERAL INFORMATION:
                                                                                                                                                              APPLICANT: McDonnell, Peter C
APPLICANT: McNulty, Dean E
APPLICANT: Rosen, Craig A
APPLICANT: Siemens, Ivo R
APPLICANT: Young, Peter R
APPLICANT: Yue, Tian-Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: SITE
                                                                      TITLE OF INVENTION: Smooth Muscle Cell-Derived Migration Factor NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                              APPLICANT:
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ID NO 37
NGTH: 985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         690 TTTGGCAACCTGAGAAGCCCTGGATGGCCAGATAACTACGACAATGACNAGGATTGCNCC 631
                                                                                                                                                                                                                                                                                                                                                                                                               630 GTTACTCTCACAGCCCCCAGAACCAY 604
                   STREET: 709 Swedeland CITY: King of Prussia STATE: PA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 PheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArgArg 31
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19406
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76.00
62.07%
51.72%
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Matches:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                    Patent No. 5916758
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO:
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                           NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                     APPLICANT: Hurle, Mark R
APPLICANT: McDonnell, Pet
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REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
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APPLICATION NUMBER: 08/5
FILING DATE: 28-NOV-1995
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                             TITLE OF INVENTION:
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                                                                   STREET: 709 Swederand CITY: King of Prussia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/839,008 FILING DATE: 23-APR-1997
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Young, Peter R
Yue, Tian-Li
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Rosen, Craig F
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Indels:
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Conservative:
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Floppy disk

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Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Smooth Muscle Cell-Derived
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
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                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1537 base pairs
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                                                               No.:
                                                                                                                  MOLECULE TYPE:
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NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,8
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APPLICATION NUMBER: 08/563,697
FILING DATE: 28-NOV-1995
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                                                                                                                               TOPOLOGY:
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McNulty, Dean E
McNulty, Dean E
Rosen, Craig A
Siemens, Ivo R
Young, Peter R
Yung, Tian-Li
Yue, Tian-Li
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Matches:
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US-09-227-357-37/c
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Sequence 37, Application US/09227357
Patent No. 6342581
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APPLICATION NUMBER: 60/051,928
APPLICATION NUMBER: 707-08
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PTEITING DATE: 1997-08-18
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FILING DATE: 1997-08-18
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APPLICATION NUMBER: 60/
FILING DATE: 1997-08-18
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FILING DATE: 1997-08-18
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FILING DATE: 1997-07-08
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FILING DATE: 1997-08-18
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SOFTWARE: Patent In Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4360 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                               Patent No. 5916758
                                                                                                                                                                                                                                                                                                                               Sequence 8,
                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Hurle,
                                                                                                                                                                             APPLICANT:
APPLICANT:
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                                                                                                                           TITLE OF INVENTION: Smooth Muscle Cell-Derived Migration Factor NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2626
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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LOCATION:
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                                COUNTRY: US
ZIP: 19406
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                                                                STATE: PA
                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                            31 ArgTrpThrLeuThrAlaProProGlyTyrArg 41
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                                                                              CITY: King of Prussia
                                                                                                ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTCTGGGCAATTTTCTAGCCCATACTACCCTGGGAGCTATCCTAATAATGCCAGATGT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArg 30
                                                                                                                                                                                                                                                                                                                               Application US/08839008
                                                                                                                                                               Young, Peter R
Yule, Tian-Li
smooth
                                                                                                                                                                                                             McDonnell, Peter C
McNulty, Dean E
Rosen, Craig A
Siemens, Ivo R
                                                  USA
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Best Local Similarity:
Query Match:
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US-09-381-779-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-874-198-1 (1-41) x US-08-839-008-8 (1-1480)
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                                                                        ; ORGANISM: Homo sapiens US-09-381-779-1
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Alignment Scores:
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                                                                                                                                                                                     SOFTWARE: Pat
SEQ ID NO 1
LENGTH: 2492
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                                                                                                                                                                                                                                                                                                                              APPLICANT: SIMPSON, JOHN W.

TITLE OF INVENTION: METHOD FOR IDENTIFYING A NUCLEIC ACID SEQUENCE
FILE REFERENCE: Cura-8 US 15966-508
CURRENT APPLICATION NUMBER: US/09/381,779
CURRENT FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: U.S.S.N. 60/054,887
PRIOR APPLICATION NUMBER: D.S.S.N. 60/054,887
PRIOR PILING DATE: 1997-08-07
PRIOR PILING DATE: 1998-08-07
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APPLICANT:
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SEQUENCE CHARACTERISTICS:
CHAR
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                         TYPE: DNA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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PRIOR APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:
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GenCore version Copyright (c) 1993 - 2003

5.1.3 Compugen

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlp
-O=/cgn2_1/USPTO_spool/US09874198/runat_10012003_092044_2595/app_query.fasta_1.199
-O=/cgn2_1/USPTO_spool/US09874198/runat_10012003_092044_2595/app_query.fasta_1.199
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=60 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09874198_6CGN_1_1_31_6runat_1001203_092044_2595 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGGUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum
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Delop 6.0
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-839-008-6
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US-08-400-159-7
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## ALIGNMENT

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RESULT 1
US-08-470-350B-1
US-08-470-350B-1
Sequence 1, Application US/08470350B
Patent No. 5684126
Patent No. 5684126

APPLICANT: Li, Xiao
APPLICANT: Snyder, Solomon H
TITLE OF INVENTION: Ebnerin: A Secreted von Ebner's Gland
TITLE OF INVENTION: Protein Associated with Taste Buds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
tein - nucleic search, using frame_plus_p2n model
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 11, 2003, 11:09:24; Search time 2190 Seconds
(without alignments)
303.203 Million cell updates/sec

Title: US-09-874-198-1
Perfect score: 238
Sequence: 1 TPLGPKWPEPVFGRLASPGF......GEYANDQERRWTLTAPPGYR 41

Scoring table: BLOSUM62

Ygapop 10.0 , Ygapext 0.5

Ygapop 10.0 , Ygapext 0.5

Ygapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Total number of hits satisfying chosen parameters:

32308132

16154066 seqs, 8097743376 residues

ched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 60 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp
-Q=/Cgn2\_1/USPTO\_spool/US098/4198/runat\_10012003\_092044\_2571/app\_query.fasta\_1.199
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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*

em\_gss\_pln:\*
em\_gss\_vrt:\*
em\_gss\_fun:\* gb\_est2: \*
gb\_htc: \*
gb\_est3: \*
gb\_est4: \*
gb\_est5: \* em\_htc:\* em\_estro:\* em\_estba:\* gb\_est1:\* em\_estpl:\* em\_estov:\* em\_estmu:\* em\_estin:\* em\_esthum:\* em\_gss\_hum:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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BQ654231 911 bp mRNA linear EST 15-JUL-2002 AGENCOURT_8493289 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6299026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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Location/Qualifiers
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Plate: LLCM2480 row: o column:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999
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/tlab_host="NH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGA6(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:6284012"
/clone_lib="NIH_MGC_100"
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/db_xref="taxon:9606"
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AGENCOURT_8299192 NIH_MGC_100
5', mRNA sequence.
BQ648641
BQ648641.1 GT:21772813
                                                                          BQ648641
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium of the Constitution of the Consortium of the I.M.A.G.E. Consortium/LLNL at:
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Tissue Procurement: CGAP (Stanford)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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BQ654231
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into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
ILRT (Life Technologies). Note: this is a NIH_MGC
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/db_xref="taxon:9606"
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1 (bases 1 to 913)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                        AGENCOURT_8188306 NIH_MGC_100
5', mRA sequence.
BQ648719
BQ648719.1 GI:21772891.
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Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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ECORI; cDNA made by Oigo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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National Institutes of Health, Mammalian

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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BQ644570
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AGENCOURT_8490607 NIH_MGC_100
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Plate: LLCM2479 row: e column:
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Tissue Procurement: CGAP (Stanford)
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1 (bases 1 to 921)
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/db_xref="taxon:9606"
/clone="IMAGE:6283375"
/clone=lib="NHI_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="PH10B (phage_resistant)"
/lab_host="PH10B (phage_resistant)"
/lab_host="PH10B (phage_resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5; adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb_Libzary constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGGGGAGTATGCCAATGACCAGGAGCGGCGCTGGACCCTGACTGCACCCCCCGGCTAC
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                                                                                                                                                                                                                                  975 bp
AGENCOURT_8488545 NIH_MGC_100 Homo
5', mRNA sequence.
BQ646367
BQ646367.1 GI:21770539
EST.
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 975)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                        Homo sapiens
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/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
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/clone="IMAGE:6293770"
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                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
                                                                                                                                                                                                                                                                                                                                      AGENCOURT_8303990 NIH_MGC_100
5', mRNA sequence:
B0653181
                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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EST.
                                                                                                                                          Unpublished (1999)
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cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be
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/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-df prining. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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/clone_lib="NIH_MGC_100"
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WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 238)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
AA896425
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                                                                                                  Unpublished (1996)
Contact: Marra M/Mouse EST Project
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/lab_host="hH10B (phage resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCACCAAC(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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Query Match:
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                                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                                                              Locus
                                                                                                                                                                   AUTHORS
 JOURNAL
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Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 197.

Location/Qualifiers
                                            Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Ishli Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishli, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Nakamura, M., Nishi, K., Sakai, C., Sakai, C., Sakai, K., Sakazume, M., Sasaki, D., Sato, K., Saito, R., Sakai, C., Sakai, K., Sakazume, M., Sasaki, D., Sato, K., Saito, R., Shiraki, T., Sogabe, Y., Suzuki, H., Togawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Wataliki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                         BB870802
BB870802
                                                                                                                                                                                                                                                                                                          mucosa, etc.
BB870802
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Unpublished (2001)
                              RIKEN Encyclopedia
                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                         house mouse.
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RIKEN full-length enriched, pooled tissues, intestinal
etc. Mus musculus cDNA clone G630025E18 5', mRNA sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6 x CBA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:1297088"
/clone_lib="Stratagene mouse
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183.00
85.37%
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                              of Mouse Full-length cDNAs (Akimura, T.,
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                 NO.:
        67
Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-171 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh, M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
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e mouse tissues.
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URL:http://genome.gsc.riken.go.jp/
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axillary lymph node, dev_stage=adult, sex=male), (tissue_type=jejunal and colic lymph node, dev_stage=adult
sex=male), (tissue_type=gall bladder, dev_stage=adult,
sex=male), (tissue_type=spinal cord, dev_stage=adult,
sex=male), (tissue_type=spinal cord, dev_stage=11 days
embryo), (tissue_type=brain, dev_stage=13 days embryo),
(tissue_type=brain, dev_stage=13 days embryo),
(tissue_type=brain, dev_stage=14 days embryo),
(tissue_type=brain, dev_stage=14 days embryo),
(tissue_type=brain, dev_stage=15 days embryo),
(tissue_type=brain, dev_stage=16 days embryo),
(tissue_type=brain, dev_stage=16 days embryo),
(tissue_type=brain, dev_stage=16 days embryo),
(tissue_type=brain, dev_stage=10 days pregnant
adult, sex=female), (tissue_type=cortex, dev_stage=10 days
neonate), (tissue_type=diencephalon, dev_stage=16 days
neonate, sex=male), (tissue_type=medulla oblongata,
dev_stage=16 days neonate, sex=male),
tissue_type=corbellum_dev_stage=16 days_neonate,
dev_stage=16 days_neonate, sex=male),
                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RIKEN full-length enriched, pooled tissues,
intestinal mucosa, etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (tissue_type=cerebellum, dev_stage=21 days neonate).
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Indels:
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Conservative:
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,Y., Tanaka,T., Mats
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The Institute of Physical and Chemical Research (I
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa
Tel: 81-45-503-9222
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Contact: Yoshihide
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e mouse tissues.
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Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer-based methods for the mouse full-length cDNA
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                            /tissue_type="gall bladder"
/dev_stage="adult"
                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="G630029B14"
                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                             /sex="male"
/note="pooled tissues ; (tissue_type=cerebellum
                                                                                                                                                  /clone_lib="RIKEN full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Itoh, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA linear I
adult male gall
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                                                                                                                                                     enriched,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci, P.,
                                                                                                                                                  adult male gall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProGlyGluTyrAlaAsnAspGlnGluArgArgTrpThrLeuThrAlaProProGlyTyr 40
                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                 WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 416)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      precursor - human ;, mRNA sequence.
W14100
W14100.1 GI:1288286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         w14100 416 bp mRNA linear EST 1 mb27h04.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:330679 5' similar to PIR:JN0883 JN0883 Ra-reactive
                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
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                                                                                                                                                                        quality sequence stop: 401.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:330679"
                                                                                                                                                         Location/Qualifiers
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VERSION
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AA237253
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA237253 546 bp mRNA linear ES mx18a07.rl Soares mouse NML Mus musculus cDNA clone IM similar to SW:CRAR_MOUSE P98064 COMPLEMENT-ACTIVATING RA-REACTIVE FACTOR PRECURSOR; mRNA sequence.
                                                                                                                                                                 Contact: Marra M/Mouse EST Project Washb-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Parkway, Box 8501, St. Ld Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                         Possible reversed clone: similarity on wrong Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 439.

Location/Qualifiers
                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                            Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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/db_xref="taxon:10090"
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                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                              WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mx15a01.rl Soares mouse NML Mus
similar to SW:CRAR_HUMAN P48740
RA-REACTIVE FACTOR PRECURSOR ;,
                            Possible reversed clone: similarity on w. Seq primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                   Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                 Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 552)
                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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              quality sequence stop: 423.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:680532"
/clone_lib="Soares mo
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/lab_host="DH10B"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 586)
1 (bases 1 to 586)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI529228 586 bp mRNA linear EST 18-MAR-1999 u161d09.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1886897 5' similar to TR:000187 000187 MASP-2 PROTEIN.;,
                                                                                                                                                                                                              Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T. Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., F., B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., F., E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                  This clone is available royalty-free through LLNL : IMAGE Consortium (info@image.llnl.gov) for further {\tt MGI:971221}
                                                                                                                                   Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence
Possible reversed clone: similarity
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                                                                          mouseest@watson.wustl.edu
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161 c 149 g 130 t 1 others
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/tissue_type="Liver"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
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/clone="IMAGE:680232"
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Seq primer:

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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arg 41
Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 600)
                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BF532409
                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                           602074450F1 NCI_CGAP_Li9
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2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: liver; Vector: pME185-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(aT) primer
was primed with an oligo(aT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1886897"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Sugano mouse
/sex="female"
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Sciurognathi; Muridae
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RESULT 16
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                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Januel: 81-45-503-9222
Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                                     Arakawa, T., Carninoi, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishi, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus
BB653589
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                     Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone_lib="NCI_CCAP_Li9"
/clone_lib="NCI_CCAP_Li9"
/clone_lib="NCI_CCAP_Li9"
/clone_lib="NCI_CCAP_Li9"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 175 c 156 g 144 t
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fikuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       further details. e mouse tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was cleaved with BamHI and XhoI. Vector: a modified pBlueScript KS(+) after bulk excision from Lambda FLC I. Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellular Biology. Elm and Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully acknowledge."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic Sciences Center and Genome Science Laboratory
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Project of Genome Exploration Research Group in Rik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN. Division of Experimental Animal Research in Riken
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/dev_stage="adult"
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/db_xref="taxon:10090"
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uj08e08.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1891334 5' similar to TR:000187 000187 MASP-2 PROTEIN. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis,
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Contact: Marra M/Mouse EST Project
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.

This is a will a few town G. Gearge B. Willow B. and This is a control of the control of
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          be used to isolate the cDNA insert. Size selection we be used to isolate the cDNA insert. Size selection we performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Traffinte of Medical Science). Custom primers for
                                                                                                                                                                                                                                                                                                                                                                                     sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACCGTGTGTG); Site_2: DraIII (CACCATGTGTG); 1st strand cDNA was primed with an oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a Draili adaptor [TGTTGGCTACTGG], digested and cloned into distinct Draili sites of the pMEIBS-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG) XhoI shou
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Best Local Similarity:
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                                                     CGC 249
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CCAGAGNAGTATGCTGACCATCAAGATCGATCCTGGACACTGACTGCACCCCCTGGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 752)
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602024289F1 NCI_CGAP_Li9
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BF233497
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9437 row: b column: 24
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                        /clone_lib="NCI_CGAP_Li9"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 218 c 186 g 168 t
                                                                                                                                                                                                                                                                                                                                                                                   /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4159415"
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RESULT 20
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Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1143 row: a column: 23
uich quality sequence stop: 767.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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/clone_Tib="NcI_CGAP_Li9"
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  EST 14-NOV-2000
NGE:4163448 5',
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                                                                                                                                                                                      21 ProGlyGluTyrAlaAsnAspGlnGluArgArgTrpThrLeuThrAlaProProGlyTyr 40
                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image:llnl.gov
Plate: LLAM9447 row: k column: 01
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National Institutes of Health, Mammalian Gene Collection (MGC)
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BF236712
BF236712.1 GI:11150598
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Location/Qualifiers
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/db_xref="taxon:10090"
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 256 c 252 g 185 t
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183.00
85.37%
78.05%
76.89%
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Matches
Conservative:
                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                     Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                00632
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-MODEL-frame+_p2n.model .DEV=xlp
-(q-/cg12_1/USPTO_spool/US09874198/runat_10012003_092043_2552/app_query.fasta_1.199
-DB=N_Geneseq_10102 .OFM97481stap .SUFFIX=p2n.rng .MINMATCH=0.1 .LOOPCL=0
-DB=N_Geneseq_10102 .OFM9748stap .SUFFIX=p2n.rng .MINMATCH=0.1 .LOOPCL=0
-LOOPEXT=0 .UNITS=bits .START=1 .END=-1 .MATRIX=blosum62 .TRANS=human40.cdi
-LIST=60 .DOCALIGN=200 .THR_SCORE=pct .THR_MAX=100 .THR_MIN=0 .ALIGN=20
-MODE=LOCAL .OUTFMT=pto .NORM=ext .HEAPSIZE=500 .MINLEN=0 .MAXLEN=200000000
-MODE=LOCAL .OUTFMT=pto .NORM=ext .HEAPSIZE=500 .MINLEN=0 .MAXLEN=2000000000
-USER=US09874198_@CGN_1_1_79_@runat_10012003_092043_2552 .NCPU=6 .ICPU=3
-NO_XUPXY .NO_MMAP .LARGEQUERY .NEG_SCORES=0 .WAIT .LONGLOG .DEV.TIMEOUT=120
-WARN_TIMEOUT=30 .THREADS=1 .YGAPOP=10 .YGAPEXT=7
-YGAPPOP=10 .YGAPEXT=0.5 .DELOP=6 .DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Ygapop 6.0 , Fgapext
Fgapop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        January 11, 2003, 11:06:19; Search time 351 Seconds (without alignments) 263.054 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
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7.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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ALIGNMENTS

RESULT 1 AAD24224 ID AAD2

AAD24224 standard; cDNA; 2472 BP.

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YARAH PAKETAN 
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and spontaneous recurrent abortion. The pharmaceutical composit comprising MASP-2 inhibitor is useful for treating inflammatory
                                                         treating infections caused by microbes such as fungus, yeast, retrovirus (e.g. human immunodeficiency virus (HTV)), or pathogenic bacteria which are resistant to at least one antibiotic medicament or multiresistant. The polynucleotide encoding MASP-2 is useful for treating patients deficient in MASP-2. The invention also discloses MASP-2 assays which are useful for determination of MASP-2 activity or levels in patients suffering from e.g. infections, inflammatory disorded the state of the suffering from e.g. infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of a polypeptide comprising amino acid sequence derived from mannan-binding lectin associated serine protease-2 (MASP-2) for producing pharmaceutical composition, to treat bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
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01-JUN-2001; 2001DK-0000870
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P-PSDB; AAE14564, AAE14568.
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(THIE/) THIEL S.
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ement fixation; infection; microbe; retrovirus; HIV; abortion;
immunodeficiency virus; pathogenic bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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82..2091
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37..81
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/note= "The last
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/transl_except= (pos:499..500, aa:His)
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                                   pharmaceutical composition
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                                                                   disorders
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        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                        WPI; 2001-639362/73.
P-PSDB; ABG21134.
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23-AUG-2000; 2000US-0649167.
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
17-MAR-2000;
19-MAY-2000;
07-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS9454 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO as for a company and the printed as the printed as the printed and the printed as the printed
                                                                                                                                                                                                                                                                                                                                                                           Human; gene therapy; neural disorder; immune system disorder; nuscular disorder; reproductive disorder; gastrointestinal dipulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation; ss.
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Match:
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                 2000US-184664P.
2000US-186350P.
2000US-19874P.
2000US-199076P.
2000US-199123P.
2000US-205515P.
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              2000US-233064P

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2000US-234223P

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2000US-236367P

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06-DEC-2000;
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01-NOV 2000;
08-NOV 2000;
                                     The present invention provides human cDNAs, proteins and related g DNAs. These can be used in the treatment of neural, inmune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascula renal and proliferative disorders and inflammation. The present se is a cDNA of the invention.
                                                                                                                                                  Claim 1;
                                                                                                                                                                                      polypeptide is used condition -
                                                                                                                                                                                                                                                              WPI; 2001-476161/51.
P-PSDB; ABB10255.
   Sequence 810 BP;
                                                                                                                                                                                                   Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a media
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L7-NOV-2000;
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     189 C;
                                                                                                                                                859pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                   MS,
     249
   G;
187 T; 4 other;
                                                                                                              proteins and related genomic
                                                                                                                                                                                                   ameliorating a medical
                                                                          cardiovascular,
                                                       present sequence
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Alignment Scores:

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AAS31599/c
ID AAS315
  В
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            24-FEB-2000
02-MAR-2000
16-MAR-2000
17-MAR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
30-JUN-2000
07-JUL-2000
07-JUL-2000
07-JUL-2000
11-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; calcium-binding protein; calcium flux; neurological disease; immune dysfunction; digestive disorder; neoplastic disease; blood disorder; infectious disease; gene therapy; immunosuppressive; antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                               WO200155304-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding novel human calcium-binding protein #23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS31599 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCWTCTGGGATTCAAAGGAGCCCGTMTGCATCGCTGCTTGCGGGGGGGGGTGATCCGCAAT
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2000US-0189874.
2000US-0199675.
2000US-0198123.
2000US-0205515.
2000US-020467.
2000US-02114886.
2000US-02114886.
2000US-02114886.
2000US-0217487.
2000US-0217487.
2000US-0217487.
2000US-0217496.
2000US-0217496.
2000US-0217496.
2000US-02250963.
2000US-0225214.
2000US-0225266.
2000US-0225266.
2000US-0225268.
2000US-0225276.
2000US-0225268.
2000US-0225268.
2000US-0225268.
2000US-0225277.
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6.15%
0.38%
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Conservative:
Mismatches:
Indels:
Gaps:
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2000US-0229343 2000US-0229344

08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

05-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SEP-2000; 08-SEP-2000; 08-SEP-2000;

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Alignment Scores: Pred. No.:
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                   proteins. Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                   neurological diseases (e.g. amylotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID), digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). To novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit
                                                                                                                                                                                                                                    The present invention relates to the isolation of novel human calcium-binding proteins (AAU19892-AAU19959), and CDNA and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include
                                                                                                                                                                                                                                                                                                                                   used
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17-NOV-
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                                              Sequence 810
                                                                                                                  activities mediated by calcium-binding proteins. The polynucleotides the invention are also useful in gene therapy. AAS31577-AAS31654 represent cDNA sequences encoding for the novel human calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-
                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecule encoding
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DB; AAU19914.
                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN GENOME
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2000US-0251990.
2000US-0254097.
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2000US-0249208.
2000US-0249209.
2000US-0249210.
2000US-0249211.
2000US-0249212.
2000US-0249213.
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2000US-0246611.
2000US-0246613.
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                                              BP; 181 A; 189
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2000US-0250391
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2000US-0249215
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                                                                                                                                                                                                                                                                                                                               le encoding a calcium-binding protein or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                        SM;
                                                                                                                                                                                                                                                                                                          English.
                                              249
Length:
Matches:
                                              <u>G</u>;
                                              187
                                              ..
                                              4
                                              other;
810
21
                                                                                part of the printed directly from WIPO
                                                                                                                  calcium-binding
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                                                                                                                                           of.
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-NOV-2000;

2000US-0246476. 2000US-0246477. 2000US-0246478. 2000US-0246523. 2000US-0246524. 2000US-0246526. 2000US-0246526. 2000US-0246527. 2000US-0246527. 2000US-0246528. 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 01-NOV-2000;

2000US-0241808. 2000US-0241809. 2000US-0241826. 2000US-0244617.

2000US-0246474 2000US-0246475 02-0CT-2000; 02-0CT-2000; 02-0CT-2000; 13-0CT-2000; 13-0CT-2000;

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:

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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
 11-JUL-2000
14-JUL-2000
26-JUL-2000
26-JUL-2000
14-AUG-2000
14-AUG-2000
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14-AUG-2000
14-AUG-2000
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04-FEB-2000;

24-FEB-2000;

02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperprolliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food addition for the process of the proliferation; skin aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2001; 2001WO-US01332
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                                                                                                                                                                                                                                                                                                                                                 16-MAR-2000;
17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel central nervous system protein #167.
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587/c
ABK43587 standard;
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 2000US-0180628.
2000US-0186340.
2000US-0189874.
2000US-0198123.
2000US-0198123.
2000US-0209467.
2000US-0209467.
2000US-0215135.
2000US-0215135.
2000US-0214647.
2000US-0217488.
2000US-0217489.
2000US-0217489.
2000US-0217489.
2000US-0217489.
2000US-0217489.
2000US-0217489.
2000US-0217489.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225214.
2000US-0225268.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451
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     22-AUG-2000
23-AUG-2000
30-AUG-2000
01-SEP-2000
01-SEP-2000
05-SEP-2000
06-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
11-SEP-2000
11-SEP
2000US-0234223

2000US-0234274

2000US-0234998

2000US-0235834

2000US-0235834

2000US-0235836

2000US-0236367

2000US-0236367

2000US-0236302

2000US-0236302

2000US-0236302

2000US-0237039

2000US-0237039

2000US-0237039

2000US-0237039

2000US-0240960

2000US-0241785

2000US-0241785

2000US-02441786

2000US-02441786

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2000US-02446174

2000US-02446174

2000US-0246477

2000US-0246524

2000US-0246525

2000US-0246525
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2000US-0225447.
2000US-0225757.
2000US-0225758.
2000US-0225759.
2000US-0226279.
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2000US-0229513

2000US-0230437

2000US-0231243

2000US-0231244

2000US-0231244

2000US-0231414

2000US-0231414

2000US-0231401

2000US-0233080

2000US-023398

2000US-023398

2000US-023398

2000US-023398

2000US-0233401

2000US-0233401

2000US-0233401

2000US-0233401

2000US-0233401

2000US-0233401

2000US-0233401

2000US-0233401

2000US-0233063

2000US-0233063
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The invention describes an isolated nucleic acid molecule (I) encoding a convel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative cdisorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, cardiovascular disorders e.g. Alzheimer's disease and campiogenesis, nervous system disorders e.g. Alzheimer's disease and campiogenesis, nervous system disorders e.g. Alzheimer's disease and campiotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired inmunodeficiency virus (AIDS) and fungi, ocular disorders e.g. acquired infection, gastrointestinal disorders e.g. dysphagia, corneal infection, gastrointestinal disorders e.g. diabetes can pluntary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, crespiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cacute kidney failure and blood related disorders e.g. myocardial cordinal cellure of primary tissnes. to recenerate tissues and in chemotaxis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 177; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NOV-2000;
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New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used food additives or preservatives as

regenerate tissues and in chemotaxis.

mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo diagnostic, forensic, gene therapy and chromosome mapping procedu

mapping procedures

The present sequence is one of a large number of 5' ESTs derived from

Claim

1; SEQ ID 1733; 71pp + CD-ROM; English.

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RESULT 6
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Best Local Similarity:
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                                                                                                                                                                                                          Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                         EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                        Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                          Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides can also be used as a food additive or preservative to
                                                                                                                                                                                                                                                 26-FEB-1999;
                                                                                                                                                                                                                                                                   21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                             gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                 AAC01735;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC01735 standard;
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                                                                                                                                                                                                                             (GEST ) GENSET
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DB; AAG01729.
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                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                             chromosome mapping;
                                                                                                                                                                                                                                                                                                                                             expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                          protein 5'
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39.29%
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                                                                                                                                                                                                          Giordano
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RESULT 7
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ID AACC
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Best Local Similarity:
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           The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 225; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                        diagnostic, forensic,
                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET
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chromosome mapping; ss.
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39.08$
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                                                                                                                                                                                                                                                                                                                      gene therapy and chromosome mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted protein; cDNA isolation;
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14
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                      30-MAR-2000;
14-APR-2000;
20-APR-2000;
28-APR-2000;
                 Claim
                                                                      New polypeptide for treating autoimmune disorders, compris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; protease; PRTS; gastrointestinal disorder; peptic esophagitis; indigestion; gastritis; cardiovascular disorder; reproductive disorder; hypertensive heart disease; myocardial infarction; autoimmune disorder; inflammatory disorder; rheumatoid arthritis; cell proliferative disorder; arteriosclerosis; cancer; epithelial disorder; eczema; endometriosis; neurological disorder; Huntington's disease; ss.
                                                    polynucleotides
                                                                                                                               P-PSDB;
                                                                                                                                                   WPI; 2001-611509/70
                                                                                                                                                                                                      Au-Young J, Bandman O, Lal
Tang YT, Burford N, Baughn
                                                                                                                                                                                                                                           Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W0200171004-A2
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                                                                                                                                                                                      Hafalia A,
                                                                                                                                                                                                                                                                                    (INCY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding protease PRTS-1.
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                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-2001; 2001WO-US08441
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••
                                                                                                                             AAB47559
                                                                                                                                                                                                                                                                                  INCYTE GENOMICS
                                                                                                                                                                                                                                             Lu DAM,
               Page 122-23;
                                                                                                                                                                                                                                                                                                                    2000US-190708P.
2000US-193182P.
2000US-197086P.
2000US-199022P.
2000US-200227P.
                                                                                                                                                                                      Lu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                       Policky JL,
Aman O, Lal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 86..2272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "PRTS-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
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93.00
67.74%
45.16%
39.08%
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                                                                                                                                                                                        Patterson
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             129pp; English
                                                                    reating gastrointestinal, cardiovascular and comprises novel human proteases (PRTS) and
                                                                                                                                                                                                                                                                                  INC
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                                                                                                                                                                                    C, MR,
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                                                                                                                                                                                                                                           Delegeane AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                       Borowsky ML,
                                                                                                                                                                                                      Nguyen DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches: Indels:
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Conservative:
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                                                                                                                                                                                                                                         Tribouley CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other;
                                                                                                                                                                                                        Gandhi AR, Hillm
Yao MG, Walia NK,
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Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAH43512-22 encode novel human proteases PRTS-1 to -11. These proteases can be administered in pharmaceutical compounds for the treatment of diseases or conditions associated with decreased expression of functional protease. Disorders which can be treated include gastrointestinal (peptic esophagitis, indigestion and gastritis), cardiovascular (hypertensive heart disease, myocardial infarction), autoimmune/inflammatory (rheumatoid arthritis), cell proliferative (arteriosclerosis, cancers), epithelial (eczema), neurological (Huntington's disease), and reproductive (endometriosis) disorders. The protein encoded by this sequence shows homology with the human precursor of P100 serine protease of Ra-reactive factor.
                                                                                                                                                                                                                                                                                                                                                                                            Mannan-binding lectin associated serine protease-3; MASP-3; MBL; human; mannan-binding lectin; complement; infection; cancer; cytostatic; immunomodulator; neuroprotective; anticonvulsive; antirheumatic; antiarthritle; antianemic; antiinflammatory; antipsoriatic; antidiabetic; antiatherosclerotic; ds.
                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human serine protease MASP-3 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF83985 standard;
Novel pure mannan-binding lectin associated serine protease
                                P-PSDB; AAB85060
                                                                                                                                                   02-DEC-1999;
21-JUL-2000;
                                                                                                                                                                                                30-NOV-2000; 2000WO-DK00659
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                                              WPI; 2001-374820/39.
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                                                                           Jensenius JC,
                                                                                                       (JENS/) JENSENIUS J C.
(THIE/) THIEL S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 ArgTrpThrLeuThrAlaProProGlyTyrArg
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                                                                                                                                                                                                                                                                                                                                                                 sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGTTTGGCCAGATCCAGTCGCCTGGTTATCCAGACTCCTATCCCAGTGATTCAGAGGTG
                                                                                                                                                 2000DK-0001126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                            Thiel S;
                                                                                                                                                                 99DK-0001721.
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
91..2277
                                                                                                                                                                                                                                                                                        /product= "MASP-3"
                                                                                                                                                                                                                                                                                                       /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.264
93.00
67.74%
45.16%
39.08%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
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Matches:
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immune system and reproductive system. The MASP-3 polypeptide is also used for treating diseases associated with human immunodeficiency virus, multiple sclerosis, myasthenia gravis, epilepsy, rheumatoid arthritis, vasculitis, autoimmune hemolytic anemia, Crohn's disease, asthma, diabetes, psoriasis, multiple myeloma, atherosclerosis etc. It is also
                                                  inflammatory condition related to complement activation through MBL/MASP complexes. MASP-3 is also useful for treating an inflammatory condition resulting from an autoimmune condition after acute myocardial infarction or brain ischemia. It is also useful for treating an individual suffering from a disorder resulting from an imbalanced cytokine network. The present sequence represents a DNA encoding a human MASP-3 polypeptide.
                                                                                                                                                                                                                        diabetes, psoriasis, multiple myeloma, atherosclerosis etc. It is all useful for inhibiting activation of C4 complement by inhibiting the pathway, inhibiting MASP-2 activity, inhibiting or treating an
                                                                                                                                                                                                                                                                                                                                                                                                                        and directly activates complement system through binding to MBL. The MASP-3 polypeptides, polynucleotides and modulators are useful for preparing a pharmaceutical composition for treating aberrant MASP-3 activity such as infections, cancer, MBL-deficiency, disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides and polynucleotides encoding the protein, used for treating reoxygenated ischemic tissues, mannon-binding lectin deficiency, multiple sclerosis -
Sequence 3895 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a mannan-binding lectin protease-3 (MASP-3) polypeptide. MASP-3 exerts an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 18; Page 88-96; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the complement activation particularly when bound to MBL/MASP-2 complexes
952 A; 1068 C;
987 G; 888
T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MBL) associated serine n inhibitory effect on
                                                                                                                                                                                                                                                        MBL
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В Qy В δõ US-09-874-198-1 (1-41) x AAF83985 Query Match: Best Local Percent Similarity: No.. 169 ATGTTTGGCCAGATCCAGTCGCCTGGTTATCCAGACTCCTATCCCAGTGATTCAGAGGTG 229 ACTTGGAATATCACTGTCCCAGATGGGTTTCGG 11 ValPheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArg 31 ArgTrpThrLeuThrAlaProProGlyTyrArg Similarity: 0.267 93.00 67.74% 45.16% 39.08% (1-3895) Matches: Conservative: Mismatches: Indels: Gaps: 261 41 3895 14 7 7 10 0

228 30 Alignment Scores:

RESULT 10 AAF74442 AAF74442 standard; cDNA; 1988

AAF74442;

Human PRO11 nucleotide sequence SEQ ID NO:21

(first entry)

Human; PRO; PROX; cytostatic; immunomodulatory;
gene therapy; cell proliferation; differentiation immune associated disorder; gestational disease; pre-clampsia; proliferation; differentiation disorder; reproduction;

Homo sapiens.

WO200110902-A2

15-FEB-2001

11-AUG-2000; 2000WO-US21857

11-AUG-1999; 10-AUG-2000; 2000US-0148433 9908-0148433

(CURA-) CURAGEN CORP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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                                                                                               WO200110902-A2
                                                                                                                                                                           Human; PRO; PROX; cytostatic; immunomodulatory; reproduction;
gene therapy; cell proliferation; differentiation disorder; c
                                                                                                                                                                                                                                                           09-MAY-2001
                                                                                                                                                                                                                                                                                           AAF74440;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator cactivity or of latency or predisposition to a.PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8;
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11-AUG-1999;
                              11-AUG-2000; 2000WO-US21857
                                                                                                                                                                                                                             Human PRO9 nucleotide
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                                                              15-FEB-2001.
                                                                                                                                                                                                                                                                                                                         AAF74440 standard; cDNA; 2127
                                                                                                                                                                                                                                                                                                                                                                                         504 TGTCACTGGCTGCTTGAGGCTCCTGAGGGCCAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                       30
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                                                                                                                                                                                                                                                                                                                                                                                                                    ArgArgTrpThrLeuThrAlaProProGlyTyrArg 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProLysTrp-----ProGluProVal-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----PheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGlu
                                                                                                                                                             associated disorder;
                                                                                                                                                                                                                                                         (first entry)
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9905-0148433
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46.15%
40.38%
38.45%
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                                                                                                                                                           gestational disease; pre-clampsia;
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Indels:
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RESULT 12
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX associated disorder, e.g. a cell proliferation and/or differentiation disorder.
                                                                                                                                                                                                  09-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding secreted polypeptides, polypeptides, useful for treating a syndrome a PROX-associated disorder, e.g. cancer -
                                            WO200110902-A2
                                                                                                                    Human; PRO; PROX; cytostatic; immunomodulatory; reproduction;
gene therapy; cell proliferation; differentiation disorder; c
                                                                                                                                                                  Human PRO10 nucleotide sequence SEQ ID NO:19.
                                                                                                                                                                                                                                                           AAF74441
                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
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                                                                                                                                                                                                                                                           standard; cDNA;
                                                                                                                                                                                              (first entry)
                                                                                                     disorder; gestational disease; pre-clampsia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        x AAF74440 (1-2127)
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91.50
46.15%
40.38%
38.45%
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Matches:
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AAF74443
ID AAF7
XX
AC AAF7
XX
DT 09-P
XX
Huma
KW Huma
KW Gena
KW Gena
KW Homm
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder (e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator cactivity or of latency or predisposition to a PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1384 CCCTTCTGGGATTCAAAGGAGCCCGTCTGCATCGCTGCCTTGCGGCGGAGTGATCCGCAAT 1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1504 TGTCACTGGCTGCTTGAGGCTCCTGAGGGCCCAGCGG 1539
                                                                                                                                                          Human; PRO; PROX; cytostatic; immunomodulatory; reproduction; gene therapy; cell proliferation; differentiation disorder; c
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      WO200110902-A2
                                                                   Homo sapiens
                                                                                                                                                                                                                                                            Human PRO12 nucleotide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF74443 standard;
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10-AUG-2000; 2000US-0148433.
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                                                                                                                         associated disorder; gestational disease; pre-clampsia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB70540
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40.38%
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Indels:
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Conservative:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
        Human; PRO; PROX; cytostatic; immunomodulatory; reproduction; gene therapy; cell proliferation; differentiation disorder; cimmune associated disorder; gestational disease; pre-clampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17) propertides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a
                                                                                                                                                                                                                                                                                                          1444 GGCACCACCGCCATCGTCTCCCAGGCTTCCCGGGCAACTACAGCAACAACCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder
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                                                                              Human
                                                                                                           09-MAY-2001
                                                                                                                                                                          AAF74438 standard; cDNA; 3863
                                                                                                                                                                                                                                            1504 TGTCACTGGCTGCTTGAGGCTCCTGAGGGCCAGCGG 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2143 BP;
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PROX-associated disorder, e.g. cancer
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10-AUG-2000;
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DB; AAB70542.
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                                                                                                                                                                                                                                                                                                                                          -----PheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGlu
                                                                              PRO7
                                                                          nucleotide sequence
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2000US-0148433
                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         x AAF74443 (1-2143)
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91.50
46.15%
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                                                                            SEQ
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pre-clampsia;

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AAF74439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide when X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder.
                              Human PRO8 nucleotide sequence SEQ ID NO:15
                                                             09-MAY-2001
                                                                                                                          AAF74439 standard;
                                                                                                                                                                                                                                               1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (e.g. cancer or immune associated disorders) and a gestational disease (e.g. pre-clampsia). They are also used for screening for a modulator of activity or of latency or predisposition to a PROX-associated disorder. AAF74432 to AAF74448 encode the specifically claimed human PROX polypeptides PRO1 to PRO17 given in AAB70531 to AAB70547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 24-27; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding secreted polypeptides, designated PROX polypeptides, useful for treating a syndrome associated with a PROX-associated disorder, e.g. cancer -
                                                                                             AAF74439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention
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10-AUG-2000; 2000US-0148433
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                                                                                                                                                                                                                                                                            ----PheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGlu
                                                                                                                                                                                                                                                                                                          ArgArgTrpThrLeuThrAlaProProGlyTyrArg 41
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 PRO;
PROX; cytostatic; immunomodulatory; reproduction;
                                                            (first entry)
                                                                                                                          cDNA; 3879
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Indels:
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy, and as PROX antagonists and PROX agonists. PROX polypeptides, nucleic acids and antibodies are useful in the manufacture of a medicament for treating a syndrome associated with a PROX-associated disorder, e.g. a cell proliferation and/or differentiation disorder (e.g. cancer or immune associated disorders) and a gestational disease
                                              ABK28635;
                                                                            ABK28635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 28-31; 166pp; English.
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10-AUG-2000; 2000US-0148433.
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                                                                                                                                                                                                                                                            CCCATCTGGGATTCAAAAGGAGCCCGTATGCATCGCTGCTTGCGGCGGAGTGATCCGCAAT 1443
                                                                                                                                                                ArgArgTrpThrLeuThrAlaProProGlyTyrArg 41
                                                                                                                                                                                                                                                                                         ProLysTrp-----ProGluProVal-----
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                                                                                                                                                                                                GCCACCACCGGCCGCATCGTCTCCCAGGCTTCCCGGGCCAACTACAGCAACAACCTCACC 1503
                                                                                                                                                                                                                -----PheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGlu 29
                                                                          standard;
               (first entry)
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                                                                          CDNA; 4034
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Conservative:
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755 T; 1 other;

3879 21 3 13 15 2

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The present invention describes isolated nucleic acids encoding secreted polypeptides, designated PROX polypeptides (i.e. a PRO polypeptide where X is an integer from 1 to 17). PROX polypeptides have cytostatic, immunomodulatory and reproduction activities, and can be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding secreted polypeptides, designated PRO) polypeptides, useful for treating a syndrome associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy; cell proliferation; differentiation disorder; cancer;
immune associated disorder; gestational disease; pre-clampsia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  designated PROX
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Human

cDNA encoding

secreted potein SECP2.

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                                                                                         Percent Similarity:
Best Local Similarity:
                               US-09-874-198-1 (1-41)
                                                                                                                                                         Alignment
                                                                                                                                                                                                                            The invention relates to forty four human secreted proteins (referred to SECP-14) and the nucleic acids encoding them. Also included are a host cell transformed with the nucleic acid, a transgenic animal comprising the nucleic acid, an anti-SECP antibody, use of the SECP proteins in isolating agonists and antagonists of SECP activity and a method of isolating compounds which alter the expression of the SECP nucleic acid. The SECP polynocleotides and CC polypeptides are useful in the diagnosis, treatment and prevention of CC cardiovascular (e.g. atherosclerosis, hypertension, myocardial CC infarction), autoimmune/inflammatory (e.g. acquired immunodeficiency syndrome (AIDS), allergies, rheumatoid arthritis), cell proliferative CC (e.g. cancer), developmental (e.g. Duchenne and Becker muscular CC disorders. Numerous other examples of each disorder are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUN-2000;
23-JUN-2000;
27-JUN-2000;
31-JUL-2000;
08-SEP-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunosuppressive; antiviral; anti-HIV; antiarthritic; antirheumatic; muscular active general; anticonvulsant; nootropic; neuroprotective; antiallergic; hypotensive; cardiovascular disorder; atherosclerosis; hypertension; myocardial infarction; autoimmune disorder; inflammatory disorder; AIDS; acquired immunodeficiency syndrome; allergy; rheumatoid arthritis; cell proliferative disorder; cancer; developmental disorder; Duchenne muscular dystrophy; neurological disorder; epilepsy; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-090431/12.
P-PSDB; AAU81976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200198353-A2
                                                                                                                                                                                                                       specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Walia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-2001; 2001WO-US19862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ramkumar J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE GENOMICS INC.
                                                                                                                                          No . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rty four human secreted proteins (referred to as SECP-1 to SECP-44), eful in the diagnosis, treatment and prevention of cardiovascular eq. atherosclerosis), autoimmune/inflammatory (e.g. allergies) and
ProLysTrp----ProGluProVal----
                                                                                                                                                         Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferative disorders
                                                                                                                                                                                        4034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 166-167; 195pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J, Tang YT, Yue H, Ell.
J, Lal P, Xu Y, Warren
Batra S, Burford N, S
Gandhi AR, Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene;
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2000US-213466P.
2000US-2140P.
2000US-222372P.
2000US-231435P.
2000US-232889P.
                                                                                                                                                                                                                      The present
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                               x ABK28635
                                                                                                                                                                                        840 A;
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91.50
46.15%
40.38%
38.45%
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                                                                                                                                                                                        1305
                                                                                                                                                                                                                      sequence
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Warren BA, Hafalia AJ
ord N, Yao MG, Nguyen
Oung J, Patterson C;
                               (1-4034)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                        1062 G;
                                                                                                                        Length: Matches:
                                                            Gaps:
                                                                            Mismatches:
Indels:
                                                                                                           Conservative:
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Hafalia AJA,
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21
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                                                                                                                                                                                        other;
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                                                                                                                                                                                                                    protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vasotropic; neuronal growth; growth factor-mediated chemotaxis; trauma; neurological disorder; muscular dystrophy; muscle injury; vulnerary; amyotropic lateral sclerosis; multiple sclerosis; ischaemia; diabetes; epilepsy; Parkinson's disease; sexual development; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1337
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                                The invention relates to an isolated human SEZ6 (hSEZ6) its corresponding DNA molecule. SEZ6 is useful for enhan
                                                                                           infertility,
                                                                                                 Novel human SEZ6 polypeptide useful for inducing neural regeneration, inhibiting neural degeneration, preventing seizures, and for treating infertility, Alzheimer's disease, stroke, seizures, Huntington's
                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; SEZ6; neural regeneration; seizure; infertility; gene therapy; stroke; Alzhelmer's disease; Huntington's disease; myasthenia gravis; nootropic; neuroprotective; anticonvulsant; cerebroprotective; stroke
                                                                    Claim
                                                                                                                                                   P-PSDB;
                                                                                                                                                             WPI; 2002-082840/11
                                                                                                                                                                                    Su EW;
                                                                                                                                                                                                                                 28-APR-2000; 2000US-200200P
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                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD25344;
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                                                                                                                                                                                                                                                                                                    WO200183552-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               impotence;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----PheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGlu
                                                                  13; Page 117-118; 127pp; English
                                                                                                                                                   AAE15853, AAE15854.
                                                                                                                                                                                                          LILLY & CO ELI
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191..2749
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191..262
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263..2749
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ID NO: 2 in o
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4198
                                                                                                                                                                                                                                                                                                                                                                                                                               "Human SEZ6 protein"
                                                                                                                                                                                                                                                                                                                                                                        "Mature hSEZ6
                                                                                                                                                                                                                                                                                                                         s region is specifically claimed claim 13 of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                       protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1372
                                enhancing
                                polypeptide a
ncing neuronal
                                                                                                                                                                                                                                                                                                                                      as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stroke;
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growth, neurite outgrowth, neuronal regeneration, neuronal growth factor-mediated chemotaxis, altered behavioural patisleep or eating disorders and for treating neurological dis

survival,

e.g.

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RESULT 18
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WPI; 2001-656860,
'P-PSDB; ABB66180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease. SEZ6 is useful for treating a patient suffering from a neurological disorder such as epilepsy, Alzheimer's disease, Parkinson disease, seizure related disorder or a disorder associated with stroke SEZ6 DNA is useful as probes for gene mapping and for detecting transcription, translation and/or expression of hSEZ6 polypeptide in human tissue. A transgenic animal is useful as an animal model in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL10283 standard; cDNA; 9455
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                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster expressed polynucleotide SEQ ID NO 25331
                                                                                  Venter JC,
                                                                                                                                                                                            23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           techniques.
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                            2001-656860/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCACCACCGGCCGCATCGTCTCTCCAGGCTTCCCGGGCAACTACAGCAACAACCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PheGlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGlu
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                                                                                  Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid genes from Drosophila and interactions -
        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
                                                                                                                                                  23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                           23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                 WO200171042-A2
                                                                                                                                                                                                                                                                           Drosophila melanogaster
                                                                                                                                                                                                                                                                                                     pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 25328
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                                                                                                                                                                                                                                                                                                                                                                                                     ABL10282;
                                                                                                                                                                                                                                                                                                                                                                                                                               ABL10282 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 25331; 21pp + Sequence Listing; English
                                                                                                                       (PEKE ) PE
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                                                                  2001-656860/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArgArgTrp
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                                                                                            JC,
                                                                                                                       CORP
                                                                                            Adams M,
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                             PWD,
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL101840-ABL16175) and the encoded proteins (ABB101840-ABL16175) and the encoded proteins

ion reagent
The invention i

is

Claim 1; SEQ ID NO 25328; 21pp + Sequence Listing; English

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RESULT 20
ABK63805
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                                                                                                                02-NOV-2000;
11-MAY-2001;
15-MAY-2001;
22-MAY-2001;
06-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3161
                                                                                                                                                                                                                                                                                                     Rat sequence differentially expressed in response to a hepatotoxin #1712
                                                                                                                                                                                                              07-FEB-2002
                                                                                                                                                                                                                                  WO200210453-A2
                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                         differential expression;
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Local Similarity:
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Predicting toxic effects of compounds or the progression of these toxic
                      WPI; 2002-241625/29
                                          Mendrick D,
                                                                                                                                                                     31-JUL-2000;
                                                                                                                                                                                         30-JUL-2001; 2001WO-US23872.
                                                                                                                                                                                                                                                                                                                             18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                      ABK63805 standard; cDNA; 4344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyArgLeuAlaSerProGlyPheProGlyGluTyrAlaAsnAspGlnGluArgArgTrp
                                                                                                                                                                                                                                                                                     ss; hepatotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                          ThrLeuThrAlaProProGlyTyrArg 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCGTGCTGCGATCTCCGGGCTATCCTGGTCAGGCGCGACCGGAACTCGACTGTCGCTGG 3220
                                                                GENE
                                                                                                                2000US-244880P.
2001US-290029P.
2001US-290645P.
2001US-292336P.
2001US-295798P.
                                                                                                                                                                                                                                                                                                                            (first entry)
                                           Porter
                                                                LOGIC INC
                                                                                    2001US-303459P
                                                                                             2001US-297457P
2001US-298884P
                                                                                                                                                                     2000US-222040P
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                                           W.
                                                                                                                                                                                                                                                                        expressed sequence tag; EST; drug screening;
on; centrilobular necrosis; steatosis.
                                          Johnson KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3058 C;
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                                          Castle
                                          ΑL,
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                                          Elashoff MR;
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Sequence 4344 BP;

1035 A; 1099

C; 1103 G; 1107 T; 0 other;

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The method can also be used to identify an agent which modulates the toxic response and predict cellular pathways that a compound modulates in a cell. The methods utilise a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, and a user interface to view the information used to present information identifying the expression level in a tissue or cell of at least one gene listed in the specification. The method is useful for elucidating global
                                          changes in gene expression and for identifying toxicity markers in tissues or cell exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression in a tissue or cell sample exposed to the compound of two or more genes listed in the specification, where differential expression the genes is indicative of at least one toxic effect or progression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comprising detecting the level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      compounds or the progression of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to methods for predicting toxic effects
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                                                        2626
2686
                                                                                                               2566 GGTCCAGTTTGGACAAGTCCTCCTTTTGTAAACTATACTTGTGGAGGTTTCCTGACTGGA 2625
                                                                                                                                                                                                                                                                                NO::
                            31
                                                                                                                                           4 GlyProLysTrpProGluProValPhe-----
TTGTGGAACATTGAAGTCCCAAACAACTACCGC 2718
                                                        CTCTCTGGGCAATTTTCTAGCCCATACTACCCTGGGAGCTATCCTAATAATGCCAGATGT
                         ArgTrpThrLeuThrAlaProProGlyTyrArg 41
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